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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated SRT nucleic acid molecules, which encode novel SRT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SRT nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SRT proteins, mutated SRT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SRT genes in this organism.

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**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
RESISTANCE AND TOLERANCE PROTEINS**

Related Applications

- 5 This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/142692, filed July 1, 1999, and also to U.S. Provisional Patent Application Serial No. 60/151214, filed August 27, 1999. This application also claims priority to German Patent Application No. 19930429.7, filed July 1, 1999, German Patent Application No. 19931413.6, filed July 8, 1999, German Patent Application No. 19931457.8, filed July 8, 1999, German Patent Application No. 19931541.8, filed July 8, 1999, German Patent Application No. 19932209.0, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932914.1, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, and 15 German Patent Application No. 19941382.7, filed August 31, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein in their entirety by this reference.

Background of the Invention

- 20 Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic 25 compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have 30 been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as stress, resistance and tolerance (SRT) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SRT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the SRT nucleic acids of the invention, or modification of the sequence of the SRT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SRT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SRT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

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Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SRT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, permitting *C. glutamicum* to survive in a setting which is
5 either chemically or environmentally hazardous to this microorganism. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*,
10 *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals, through the ability of these proteins to permit growth and multiplication of *C. glutamicum* (and also continuous production of one or more fine
15 chemicals) under circumstances which would normally impede growth of the organism, such as those conditions frequently encountered during large-scale fermentative growth. For example, by overexpressing or engineering a heat-shock induced protease molecule such that it is optimized in activity, one may increase the ability of the bacterium to degrade incorrectly folded proteins when the bacterium is challenged with high
20 temperatures. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins to interfere with normal reaction mechanisms in the cell, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in yield, production, and/or efficiency of
25 production of one or more desired fine chemicals, due at least to the relatively greater number of cells producing these chemicals in the culture.

This invention provides novel SRT nucleic acid molecules which encode SRT proteins which are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism.
30 Nucleic acid molecules encoding an SRT protein are referred to herein as SRT nucleic acid molecules. In a preferred embodiment, the SRT protein participates in metabolic pathways permitting *C. glutamicum* to survive in a setting which is either chemically or

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environmentally hazardous to this microorganism. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SRT protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SRT-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SRT activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or

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more homologous to an amino acid sequence of the invention (e.g., an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7...)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an SRT fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (e.g., a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and has the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or possesses one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (e.g., a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SRT protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, e.g., recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SRT protein by culturing the host cell in a suitable medium. The SRT protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SRT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by the introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SRT sequence as

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a transgene. In another embodiment, an endogenous SRT gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SRT gene. In another embodiment, an endogenous or introduced SRT gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of a SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 304)) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SRT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SRT protein or portion thereof possesses the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In another preferred embodiment, the isolated SRT protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism.

The invention also provides an isolated preparation of an SRT protein. In preferred embodiments, the SRT protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein

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which is substantially homologous to an entire amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing).). In yet another embodiment, the protein is at least about 50%,
5 preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SRT protein comprises an amino acid sequence which is at least about 50% or more homologous to
10 one of the amino acid sequences of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to improve the survival rate of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SRT protein can comprise an amino acid sequence
15 which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred
20 that the preferred forms of SRT proteins also have one or more of the SRT bioactivities described herein.

The SRT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SRT polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SRT protein alone. In
25 other preferred embodiments, this fusion protein results in increased yields, production, and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates the production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which
30 modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of an SRT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SRT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining
5 a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SRT nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

10 Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates SRT protein activity or SRT nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated in resistance to one or more
15 toxic chemicals or in resistance to one or more environmental stresses, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SRT protein activity can be an agent which stimulates SRT protein activity or SRT nucleic acid expression. Examples of agents which stimulate SRT protein activity or SRT nucleic acid expression include small
20 molecules, active SRT proteins, and nucleic acids encoding SRT proteins that have been introduced into the cell. Examples of agents which inhibit SRT activity or expression include small molecules, and antisense SRT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SRT
25 gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred
30 embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SRT nucleic acid and protein molecules which are involved in the survival of *C. glutamicum* upon exposure of this microorganism to chemical or environmental hazards. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, since these SRT proteins provide a means for continued growth and multiplication of *C. glutamicum* in the presence of toxic chemicals or hazardous environmental conditions, such as may be encountered during large-scale fermentative growth. By increasing the growth rate or at least maintaining normal growth in the face of poor, if not toxic, conditions, one may increase the yield, production, and/or efficiency of production of one or more fine chemicals from such a culture, at least due to the relatively greater number of cells producing the fine chemical in the culture. Aspects of the invention are further explicated below.

15 I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in

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Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

5 A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the
10 nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids
15 have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways.
20 to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are
25 interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout
30 the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in

both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
5 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of
10 producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-
15 step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.
20 Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction
25 catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine
30 from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of

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the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them.

5 Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount
10 of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although
15 they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other
20 processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins
25 may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such
30 molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) 'Nutrition, Lipids, Health, and Disease' Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives

of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

- 5 Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are
- 10 also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

- The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-
- 15 scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

20 C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

- Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic
- 25 structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or
- 30 their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are

nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

- Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.
- The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.

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Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Resistance to Damage from Chemicals, Environmental Stress, and Antibiotics

Production of fine chemicals is typically performed by large-scale culture of bacteria developed to produce and secrete large quantities of these molecules. However, this type of large-scale fermentation results in the subjection of the microorganisms to stresses of various kinds. These stresses include environmental stress and chemical stress.

A. Resistance to Environmental Stress

Examples of environmental stresses typically encountered in large-scale fermentative culture include mechanical stress, heat stress, stress due to limited oxygen, stress due to oxygen radicals, pH stress, and osmotic stress. The stirring mechanism used in most large-scale fermentors to ensure aeration of the culture produces heat, thus increasing the temperature of the culture. Increases in temperature induce the well-characterized heat shock response, in which a set of proteins are expressed which not

only aid in the survival of the bacterium in the face of high temperatures, but also increase survival in response to a number of other environmental stresses (see Neidhardt, F.C., *et al.*, eds. (1996) *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 1382-1399; Wosten, M. M. (1998) *FEMS Microbiology Reviews* 22(3): 127-50; 5 Bahl, H. *et al.* (1995) *FEMS Microbiology Reviews* 17(3): 341-348; Zimmerman, J.L., Cohill, P.R. (1991) *New Biologist* 3(7): 641-650; Samali, A., and Orrenius, S. (1998) *Cell. Stress Chaperones* 3(4): 228-236, and references contained therein from each of these citations). Regulation of the heat shock response in bacteria is facilitated by specific sigma factors and other cellular regulators of gene expression (Hecker, M., 10 Volker, U (1998). *Molecular Microbiology* 29(5): 1129-1136). One of the largest problems that the cell encounters when exposed to high temperature is that protein folding is impaired; nascent proteins have sufficient kinetic energy in high temperature circumstances that it is difficult for the growing polypeptide chain to remain in a stable conformation long enough to fold properly. Thus, two of the key types of proteins 15 expressed during the heat shock response consist of chaperones (proteins which assist in the folding or unfolding of other proteins – see, *e.g.*, Fink, A.L. (1999) *Physiol. Rev.* 79(2): 425-449), and proteases, which can destroy any improperly folded proteins. Examples of chaperones expressed during the heat shock response include GroEL and DNAK; proteases known to be expressed during this cellular reaction to heat shock 20 include Lon, FtsH, and ClpB.

Other environmental stresses besides heat may also provoke a stress response. Though the fermentor stirring process is meant to introduce oxygen into the culture, oxygen may remain in limited supply, particularly when the culture is advanced in growth and the oxygen needs of the culture are thereby increased; an insufficient supply 25 of oxygen is another stress for the microorganism. Cells in fermentor cultures are also subjected to a number of osmotic stresses, particularly when nutrients are added to the culture, resulting in a high extracellular and low intracellular concentration of these molecules. Further, the large quantities of the desired molecules produced by these organisms in culture may contribute to osmotic stress of the bacteria. Lastly, aerobic 30 metabolism such as that used by *C. glutamicum* results in carbon dioxide as a waste product; secretion of this molecule may acidify the culture medium due to conversion of this molecule to carboxylic acid. Thus, bacteria in culture are also frequently subjected

to acidic pH stress. The converse may also be true – when high levels of basic waste molecules such as ammonium are present in the culture medium, the bacteria in culture may be subjected to basic pH stress as well.

To combat such environmental stresses, bacteria have elegant gene systems which are expressed upon exposure to one or more stresses, such as the aforementioned heat shock system. Genes expressed in response to osmotic stress, for example, encode proteins capable of transporting or synthesizing compatible solutes such that osmotic intake or export of a particular molecule is slowed to manageable levels. Other examples of stress-induced bacterial proteins are those involved in trehalose biosynthesis, those encoding enzymes involved in ppGpp metabolism, those involved in signal transduction, particularly those encoding two-component systems which are sensitive to osmotic pressure, and those encoding transcription factors which are responsive to a variety of stress factors (*e.g.*, RssB analogues and/or sigma factors). Many other such genes and their protein products are known in the art.

15

B. Resistance to Chemical Stress

Aside from environmental stresses, cells may also experience a number of chemical stresses. These may fall into two categories. The first are natural waste products of metabolism and other cellular processes which are secreted by the cell to the surrounding medium. The second are chemicals present in the extracellular medium which do not originate from the cell. Generally, when cells excrete toxic waste products from the concentrated intracellular cytoplasm into the relatively much more dilute extracellular medium, these products dissipate such that extracellular levels of the possibly toxic compound are quite low. However, in large-scale fermentative culture of the bacterium, this may not be the case: so many bacteria are grown in a relatively small environment and at such a high metabolic rate that waste products may accumulate in the medium to nearly toxic levels. Examples of such wastes are carbon dioxide, metal ions, and reactive oxygen species such as hydrogen peroxide. These compounds may interfere with the activity or structure of cell surface molecules, or may re-enter the cell, where they can seriously damage proteins and nucleic acids alike. Certain other chemicals hazardous to the normal functioning of cells may be naturally found in the extracellular medium. For example, metal ions such as mercury, cadmium, nickel or

30

copper are frequently found in water sources, and may form tight complexes with cellular enzymes which prevent the normal functioning of these proteins.

C. Resistance to Antibiotics

- 5 Bacteriocidal proteins or antibiotics, may also be found in the extracellular milieu, either through the intervention of the researcher, or as a natural product from another organism, utilized to gain a competitive advantage. Microorganisms have several art-known mechanisms to protect themselves against antimicrobial chemicals. Degradation, modification, and export of compounds toxic to the cell are common
- 10 methods by which microorganisms eliminate or detoxify antibiotics. Cytoplasmic 'efflux-pumps' are known in several prokaryotes and show similarities to the so-called 'multidrug resistance' proteins from higher eukaryotes (Neyfakh, A. A. , *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88: 4781-4785). Examples of such proteins include *emrAB* from *E. coli* (Lomovskaya, O. and K. Lewis (1992) *Proc. Natl. Acad. Sci. USA* 89:
- 15 8938-8942), *lmrB* from *B. subtilis* (Kumano, M. *et al.* (1997) *Microbiology* 143: 2775-2782), *smr* from *S. aureus* (Grinius, L.G. *et al.* (1992) *Plasmid* 27: 119-129) or *cmr* from *C. glutamicum* (Kaidoh, K. *et al.* (1997) *Micro. Drug Resist.* 3: 345-350). *C. glutamicum* itself is non-pathogenic, in contrast to several other members of the genus *Corynebacterium* , such as *C. diphtheriae* or *C. pseudotuberculosis*. Several pathogenic
- 20 *Corynebacteria* are known to have multiple resistances against a variety of antibiotics, such as *C. jeikeium* and *C. urealyticum* (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214).

- Lincosamides are recognized as effective antibiotics against *Corynebacterium* species (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214). An
- 25 unexpected result of the present invention was the identification of a gene encoding a lincosamide-resistance protein (in particular, a lincomycin-resistance protein). The LMRB protein from *C. glutamicum* shows 40% homology to the product of the *lmrB* gene from *B. subtilis* (see Genbank accession no. AL009126), as calculated using version 1.7 of the program CLUSTALW (Thompson, J.D., Higgins, D.G., Gibson, T. J.
- 30 (1994) *Nucl. Acids Res.* 22: 4673-4680) using standard parameters (PAIRWISE ALIGNMENT PARAMETERS: slow/accurate alignments: Gap Open Penalty = 10.00, Gap Extension Penalty = 0.10, Protein weight matrix = BLOSUM 30, DNA weight

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matrix = IUB, Fast/Approximate alignments: Gap penalty = 3, K-tuple (word) size = 1, No. of top diagonals = 5, Window size = 5, Toggle Slow/Fast pairwise alignments = slow. Multiple alignment parameters: Gap Opening Penalty = 10.00, Gap Extension Penalty = 0.05, Delay divergent sequences = 40%, DNA transitions weight = 0.50, 5 Protein weight matrix = BLOSUM series, DNA weight matrix = IUB, Use negative matrix = OFF).

Environmental stress, chemical stress, and antibiotic or other antimicrobial stress may influence the behavior of the microorganisms during fermentor culture, and may have an impact on the production of the desired compound from these organisms.

10 For example, osmotic stress of a microorganism may cause inappropriate or inappropriately rapid uptake of one or more compounds which can ultimately lead to cellular damage or death due to osmotic shock. Similarly, chemicals present in the culture, either exogenously added (*e.g.*, antimicrobial compounds intended to eliminate unwanted microbes) or generated by the bacteria themselves (*e.g.*, waste compounds

15 such as heavy metals or oxygen radicals, or even antimicrobial compounds) may result in inhibition of fine chemical production or even death of the organism. The genes of the invention encode *C. glutamicum* proteins which act to prevent cell damage or death, by specifically counteracting the source or effect of the environmental or chemical stress.

20

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SRT nucleic acid and protein molecules, which increase the ability of *C. glutamicum* to survive in chemically or environmentally hazardous

25 settings. In one embodiment, the SRT molecules function to confer resistance to one or more environmental or chemical stresses to *C. glutamicum*. In a preferred embodiment, the activity of the SRT molecules of the present invention has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SRT molecules of the invention are modulated in activity, such that the

30 yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* is also modulated.

The language, "SRT protein" or "SRT polypeptide" includes proteins which participate in the resistance of *C. glutamicum* to one or more environmental or chemical stresses. Examples of SRT proteins include those encoded by the SRT genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SRT gene" or "SRT

5 nucleic acid sequence" include nucleic acid sequences encoding an SRT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SRT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given

10 time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e.,

15 fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound,

20 preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The

25 language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The terms "resistance" and "tolerance" are art-known and include the ability

30 of a cell to not be affected by exposure to a chemical or an environment which would otherwise be detrimental to the normal functioning of these organisms. The terms "stress" or "hazard" include factors which are detrimental to the normal functioning of

cells such as *C. glutamicum*. Examples of stresses include “chemical stress”, in which a cell is exposed to one or more chemicals which are detrimental to the cell, and “environmental stress” where a cell is exposed to an environmental condition outside of those to which it is adapted. Chemical stresses may be either natural metabolic waste products such as, but not limited to reactive oxygen species or carbon dioxide, or chemicals otherwise present in the environment, including, but not limited to heavy metal ions or bacteriocidal proteins such as antibiotics. Environmental stresses may be, but are not limited to temperatures outside of the normal range, suboptimal oxygen availability, osmotic pressures, or extremes of pH, for example.

10 In another embodiment, the SRT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the SRT proteins of the invention may be manipulated such that its function is modulated. The alteration of activity of stress response, resistance or tolerance genes
15 such that the cell is increased in tolerance to one or more stresses may improve the ability of that cell to grow and multiply in the relatively stressful conditions of large-scale fermentor culture. For example, by overexpressing or engineering a heat-shock induced chaperone molecule such that it is optimized in activity, one may increase the ability of the bacterium to correctly fold proteins in the face of nonoptimal temperature
20 conditions. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in the yield, production, and/or efficiency of production of one or more desired fine chemicals,
25 due at least to the relatively greater number of cells producing these chemicals in the culture.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the
30 isolated *C. glutamicum* SRT DNAs and the predicted amino acid sequences of the *C. glutamicum* SRT proteins are shown the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively.,.

Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode chemical and environmental stress, resistance, and tolerance proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (e.g., the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence. Ranges and identity values intermediate to the above-recited values, (e.g., 75%-80% identical, 85-87% identical, 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included.

The SRT proteins or biologically active portions or fragments thereof of the invention can confer resistance or tolerance to one or more chemical or environmental stresses, or may have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SRT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SRT-encoding nucleic acid (e.g., SRT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides

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of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated
5 from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SRT nucleic acid molecule can contain less than
10 about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or
15 other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SRT DNA can be
20 isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).
25 Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the
30 Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate

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extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers
5 for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and
10 characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SRT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic
15 acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SRT DNAs of the invention. This DNA comprises sequences encoding SRT proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID
20 NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5
25 digits (*i.e.*, RXA01524, RXN00493, or RXS01027). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the
30 Sequence Listing, which may be also be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an

even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA01524 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same
5 RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated RXA01524 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA01524, the amino acid sequence designated RXN00034 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule
10 RXN00034, and the amino acid sequence in designated RXS00568 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXS00568. The correspondence between the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated
15 gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:7, designated, as indicated on Table 1, as "F RXA00498", is an F-designated gene, as are SEQ ID NOs: 25, 33, and 37 (designated on Table 1 as "F RXA01345", "F RXA02543", and "F RXA02282", respectively).

20 In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version
25 relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID
30 NO: of the Sequence Listing, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence

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Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
5 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the
10 invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an
15 additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention,, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs
20 of the Sequence Listing for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SRT protein. The nucleotide sequences determined from the cloning of the SRT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SRT homologues in other cell types and organisms, as well as SRT homologues from other
25 *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-
30 numbered SEQ ID NOs of the Sequence Listing),, an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SRT homologues.

Probes based on the SRT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-
5 factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SRT protein, such as by measuring a level of an SRT-encoding nucleic acid in a sample of cells, *e.g.*, detecting SRT mRNA levels or determining whether a genomic SRT gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein
10 or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to confer resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses. As used herein, the language "sufficiently
15 homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is capable of
20 participating in the resistance of *C. glutamicum* to one or more chemical or environmental stresses. Protein members of such metabolic pathways, as described herein, function to increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical hazards or stresses. Examples of such activities are also described herein. Thus, "the function of an SRT protein" contributes to the overall
25 resistance of *C. glutamicum* to elements of its surroundings which may impede its normal growth or functioning, and/or contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SRT protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
30 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of

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the Sequence Listing). Ranges and identity values intermediate to the above-recited values, (*e.g.*, 75%-80% identical, 85-87% identical, or 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower
5 limits are intended to be included.

Portions of proteins encoded by the SRT nucleic acid molecules of the invention are preferably biologically active portions of one of the SRT proteins. As used herein, the term "biologically active portion of an SRT protein" is intended to include a portion, *e.g.*, a domain/motif, of an SRT protein that is capable of imparting resistance or
10 tolerance to one or more environmental or chemical stresses or hazards, or has an activity as set forth in Table 1. To determine whether an SRT protein or a biologically active portion thereof can increase the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as
15 detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SRT protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SRT protein or peptide (*e.g.*, by
20 recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SRT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic
25 code and thus encode the same SRT protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C.*
30 *glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

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It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00084 (SEQ ID NO:189), a nucleotide sequence which is greater than and/or at least 56% identical to the nucleotide sequence designated RXA00605 (SEQ ID NO:11), and a nucleotide sequence which is greater than and/or at least 50% identical to the nucleotide sequence designated RXA00886 (SEQ ID NO:39). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SRT nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SRT proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the SRT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SRT protein, preferably a *C. glutamicum* SRT protein. Such

natural variations can typically result in 1-5% variance in the nucleotide sequence of the SRT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SRT that are the result of natural variation and that do not alter the functional activity of SRT proteins are intended to be within the scope of the invention.

- 5 Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SRT DNA of the invention can be isolated based on their homology to the *C. glutamicum* SRT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in
- 10 another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent
- 15 conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such
- 20 stringent conditions are known to those of ordinary skill in the art in the art and can be found in Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an
- 25 isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C.*
- 30 *glutamicum* SRT protein.

In addition to naturally-occurring variants of the SRT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be

introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded SRT protein, without altering the functional ability of the SRT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a

5 nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SRT proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SRT protein, whereas an "essential" amino acid residue is required for SRT protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

10 semi-conserved in the domain having SRT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SRT activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SRT proteins that contain changes in amino acid residues that are not essential for SRT activity. Such SRT proteins differ in amino acid sequence from a sequence of

15 an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SRT activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of increasing the resistance or tolerance of *C. glutamicum* to

20 one or more environmental or chemical stresses, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95%

25 homologous to one of these sequences in, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be

30 introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one

sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SRT protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SRT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SRT coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SRT activity described herein to identify mutants that retain SRT activity. Following mutagenesis of one the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can

be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SRT proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SRT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SRT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO.: 120 (RXA00600) comprises nucleotides 1 to 1098). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SRT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SRT disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SRT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SRT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SRT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to

increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SRT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in

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which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms
5 specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

10 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to
15 catalytically cleave SRT mRNA transcripts to thereby inhibit translation of SRT mRNA. A ribozyme having specificity for an SRT-encoding nucleic acid can be designed based upon the nucleotide sequence of an SRT cDNA disclosed herein (*i.e.*, SEQ ID NO:119 (RXA00600)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the
20 nucleotide sequence to be cleaved in an SRT-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SRT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

25 Alternatively, SRT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SRT nucleotide sequence (*e.g.*, an SRT promoter and/or enhancers) to form triple helical structures that prevent transcription of an SRT gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-
30 36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SRT protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting
5 another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial
10 vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression
15 vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-
20 associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is
25 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory
30 sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,

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Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-,
5 trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, amy, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use
10 artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described
15 herein (e.g., SRT proteins, mutant forms of SRT proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SRT proteins in prokaryotic or eukaryotic cells. For example, SRT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992)
20 "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics
25 of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology*:
30 *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion
5 vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein
10 from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase
15 (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SRT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin.
20 Recombinant SRT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-
25 III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the
30 pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7

gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the SRT protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the SRT proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the SRT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (e.g., the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
5 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018).

10 In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements.
15 For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY,
20 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable
25 tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters
30 (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and

European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

5 The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SRT mRNA. Regulatory sequences operatively
10 linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid
15 or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

20 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due
25 to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SRT protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or
30 mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related

to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms

5 "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA)) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-

10 dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the

15 expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418,

20 hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SRT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

25 To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SRT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SRT gene. Preferably, this SRT gene is a *Corynebacterium glutamicum* SRT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source.

30 In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SRT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively,

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the vector can be designed such that, upon homologous recombination, the endogenous SRT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SRT protein). In the homologous recombination vector, the altered portion of the SRT gene is flanked at its 5' and 3' ends by additional nucleic acid of the SRT gene to allow for homologous recombination to occur between the exogenous SRT gene carried by the vector and an endogenous SRT gene in a microorganism. The additional flanking SRT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SRT gene has homologously recombined with the endogenous SRT gene are selected, using art-known techniques.

15 In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an SRT gene on a vector placing it under control of the lac operon permits expression of the SRT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

20 In another embodiment, an endogenous SRT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SRT gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SRT gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SRT protein. Accordingly, the invention further provides methods for producing SRT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SRT protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SRT protein) in a suitable medium until SRT protein is produced. In another embodiment, the method further comprises isolating SRT proteins from the medium or the host cell.

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C. Isolated SRT Proteins

Another aspect of the invention pertains to isolated SRT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SRT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SRT protein having less than about 30% (by dry weight) of non-SRT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SRT protein, still more preferably less than about 10% of non-SRT protein, and most preferably less than about 5% non-SRT protein. When the SRT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein having less than about 30% (by dry weight) of chemical precursors or non-SRT chemicals, more preferably less than

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about 20% chemical precursors or non-SRT chemicals, still more preferably less than about 10% chemical precursors or non-SRT chemicals, and most preferably less than about 5% chemical precursors or non-SRT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SRT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SRT protein in a microorganism such as *C. glutamicum*.

An isolated SRT protein or a portion thereof of the invention can contribute to the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to mediate the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SRT protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper

and/or lower limits are intended to be included. The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein. For example, a preferred SRT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes
5 under stringent conditions, to a nucleotide sequence of the invention, and which can increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical stresses, or which has one or more of the activities set forth in Table 1.

In other embodiments, the SRT protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of
10 the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SRT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%,
15 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which
20 has at least one of the SRT activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains
25 to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention .

Biologically active portions of an SRT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SRT protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the
30 amino acid sequence of a protein homologous to an SRT protein, which include fewer amino acids than a full length SRT protein or the full length protein which is homologous to an SRT protein, and exhibit at least one activity of an SRT protein.

Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SRT protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SRT protein include one or more selected domains/motifs or portions thereof having biological activity.

SRT proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SRT protein is expressed in the host cell. The SRT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SRT protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SRT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SRT antibody, which can be produced by standard techniques utilizing an SRT protein or fragment thereof of this invention.

The invention also provides SRT chimeric or fusion proteins. As used herein, an SRT "chimeric protein" or "fusion protein" comprises an SRT polypeptide operatively linked to a non-SRT polypeptide. An "SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to SRT, whereas a "non-SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SRT protein, *e.g.*, a protein which is different from the SRT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SRT polypeptide and the non-SRT polypeptide are fused in-frame to each other. The non-SRT polypeptide can be fused to the N-terminus or C-terminus of the SRT polypeptide. For example, in one embodiment the fusion protein is a GST-SRT fusion protein in which the SRT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SRT proteins. In another embodiment, the fusion protein is an SRT protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression

and/or secretion of an SRT protein can be increased through use of a heterologous signal sequence.

Preferably, an SRT chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the
5 different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene
10 can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel
15 *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An SRT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SRT protein.

Homologues of the SRT protein can be generated by mutagenesis, *e.g.*, discrete
20 point mutation or truncation of the SRT protein. As used herein, the term "homologue" refers to a variant form of the SRT protein which acts as an agonist or antagonist of the activity of the SRT protein. An agonist of the SRT protein can retain substantially the same, or a subset, of the biological activities of the SRT protein. An antagonist of the SRT protein can inhibit one or more of the activities of the naturally occurring form of
25 the SRT protein, by, for example, competitively binding to a downstream or upstream member of the SRT system which includes the SRT protein. Thus, the *C. glutamicum* SRT protein and homologues thereof of the present invention may increase the tolerance or resistance of *C. glutamicum* to one or more chemical or environmental stresses.

In an alternative embodiment, homologues of the SRT protein can be identified
30 by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SRT protein for SRT protein agonist or antagonist activity. In one embodiment, a variegated library of SRT variants is generated by combinatorial mutagenesis at the nucleic acid

- level and is encoded by a variegated gene library. A variegated library of SRT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SRT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SRT sequences therein. There are a variety of methods which can be used to produce libraries of potential SRT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SRT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.
- 15 In addition, libraries of fragments of the SRT protein coding can be used to generate a variegated population of SRT fragments for screening and subsequent selection of homologues of an SRT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SRT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SRT protein.
- 25 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SRT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
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vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the
5 screening assays to identify SRT homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SRT library, using methods well known in the art.

10 *D. Uses and Methods of the Invention*

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C.*
15 *glutamicum* sequences of interest; evolutionary studies; determination of SRT protein regions required for function; modulation of an SRT protein activity; modulation of the activity of an SRT pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

The SRT nucleic acid molecules of the invention have a variety of uses. First,
20 they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms
25 under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which
30 involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the

body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SRT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The resistance processes in which the molecules of the invention participate are utilized by a wide variety of cells; by comparing the sequences

of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The genes of the invention, *e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other gene of the invention encoding a chemical or environmental resistance or tolerance protein (*e.g.*, resistance against one or more antibiotics), may be used as genetic markers for the genetic transformation of (*e.g.*, the transfer of additional genes into or disruption of preexisting genes of) organisms such as *C. glutamicum* or other bacterial species. Use of these nucleic acid molecules permits efficient selection of organisms which have incorporated a given transgene cassette (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon, or other nucleic acid element), based on a trait which permits the survival of the organism in an otherwise hostile or toxic environment (*e.g.*, in the presence of an antimicrobial compound). By employing one or more of the genes of the invention as genetic markers, the speed and ease with which organisms having desirable transformed traits (*e.g.*, modulated fine chemical production) are engineered and isolated are improved. While it is advantageous to use the genes of the invention for selection of transformed *C. glutamicum* and related bacteria, it is possible, as described herein, to use homologs (*e.g.*, homologs from other organisms), allelic variants or fragments of the gene retaining desired activity. Furthermore, 5' and 3' regulatory elements of the genes of the invention may be modified as described herein (*e.g.*, by nucleotide substitution, insertion, deletion, or replacement with a more desirable genetic element) to modulate the transcription of the gene. For example, an LMRB variant in which the nucleotide sequence in the region from -1 to -200 5' to the start codon has been altered to modulate (preferably increase) the transcription and/or translation of LMRB may be employed, as can constructs in which a gene of the invention (*e.g.*, the LMRB gene (SEQ ID NO:1)) is functionally coupled to one or more regulatory signals (*e.g.*, inducer or repressor binding sequences) which can be used for modulating gene expression.

Similarly, more than one copy of a gene (functional or inactivated) of the invention may be employed.

An additional application of the genes of the invention (*e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other drug- or antibiotic-resistance gene) is in the discovery of new antibiotics which are active against *Corynebacteria* and/or other bacteria. For example, a gene of the invention may be expressed (or overexpressed) in a suitable host to generate an organism with increased resistance to one or more drugs or antibiotics (in the case of LMRB, lincosamides in particular, especially lincomycin). This type of resistant host can subsequently be used to screen for chemicals with bacteriostatic and/or bacteriocidal activity, such as novel antibiotic compounds. It is possible, in particular, to use the genes of the invention (*e.g.*, the LMRB gene) to identify new antibiotics which are active against those microorganisms which are already resistant to standard antibiotic compounds.

The invention provides methods for screening molecules which modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of SRT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SRT proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SRT protein is assessed.

Manipulation of the SRT nucleic acid molecules of the invention may result in the production of SRT proteins having functional differences from the wild-type SRT proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity. The goal of such manipulations is to increase the viability and activity of the cell when the cell is exposed to the environmental and chemical stresses and hazards which frequently accompany large-scale fermentative culture. Thus, by increasing the activity or copy number of a heat-shock-regulated protease, one may increase the ability of the cell to destroy incorrectly folded proteins, which may otherwise interfere with normal cellular functioning (for example, by continuing to bind substrates or cofactors although the protein lacks the activity to act on these molecules appropriately). The same is true for the overexpression or optimization of activity of one or more chaperone molecules

induced by heat or cold shock. These proteins aid in the correct folding of nascent polypeptide chains, and thus their increased activity or presence should increase the percentage of correctly folded proteins in the cell, which in turn should increase the overall metabolic efficiency and viability of the cells in culture. The overexpression or
5 optimization of the transporter molecules activated by osmotic shock should result in an increased ability on the part of the cell to maintain intracellular homeostasis, thereby increasing the viability of these cells in culture. Similarly, the overproduction or increase in activity by mutagenesis of proteins involved in the development of cellular resistance to chemical stresses of various kinds (either by transport of the offending
10 chemical out of the cell or by modification of the chemical to a less hazardous substance) should increase the fitness of the organism in the environment containing the hazardous substance (*i.e.*, large-scale fermentative culture), and thereby may permit relatively larger numbers of cells to survive in such a culture. The net effect of all of these mutagenesis strategies is to increase the quantity of fine-chemical-producing
15 compounds in the culture, thereby increasing the yield, production, and/or efficiency of production of one or more desired fine chemicals from the culture.

This aforementioned list of mutagenesis strategies for SRT proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By
20 these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SRT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis
25 pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents,
30 published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Genes Included in the Application

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA01524	GR00424	29041	30483	Lincomycin RESISTANCE PROTEIN
3	4	RXA00497	GR00124	52	348	10 KD CHAPERONIN
5	6	RXN00493	VW0086	14389	16002	60 KD CHAPERONIN
7	8	F RXA00498	GR00124	363	1601	60 KD CHAPERONIN
9	10	RXA01217	GR00353	802	203	GENERAL STRESS PROTEIN CTC
11	12	RXA00605	GR00159	7412	5865	CATALASE (EC 1.11.1.6)
13	14	RXA00404	GR00089	2909	594	CARBON STARVATION PROTEIN A
15	16	RXN03119	VW0098	86877	87008	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
17	18	RXN03120	VW0098	87351	87476	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
19	20	RXN00575	VW0323	14716	15252	PHOSPHOTHRICIN-RESISTANCE PROTEIN
21	22	F RXA00575	GR00156	2130	1648	PHOSPHOTHRICIN-RESISTANCE PROTEIN

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXN01345	VW0123	4883	3432	Moleculares chaperon (HSP70/DnaK family)
25	26	F RXA01345	GR00391	1172	6	Molecular chaperones (HSP70/DnaK family)
27	28	RXA02541	GR00726	13657	12473	DNAJ PROTEIN
29	30	RXA02542	GR00726	14518	13865	GRPE PROTEIN
31	32	RXN02543	VW0057	22031	20178	DNAK PROTEIN
33	34	F RXA02543	GR00726	16375	14522	DNAK PROTEIN
35	36	RXN02280	VW0152	1849	26	TRAP1
37	38	F RXA02282	GR00659	1145	1480	Molecular chaperone, HSP90 family
39	40	RXA00886	GR00242	12396	13541	DNAJ PROTEIN
41	42	RXS00568	VW0251	2928	1582	TRIGGER FACTOR
43	44	RXN03038	VW0017	42941	43666	PS1 PROTEIN VORLÄUFER
45	46	RXN03039	VW0018	2	631	PS1 PROTEIN VORLÄUFER
47	48	RXN03040	VW0018	761	1069	PS1 PROTEIN VORLÄUFER
49	50	RXN03051	VW0022	2832	3566	PS1 PROTEIN VORLÄUFER
51	52	RXN03054	VW0026	1906	3486	PS1 PROTEIN VORLÄUFER
53	54	RXN02949	VW0025	31243	31575	PREPROTEIN TRANSLOKASE SECE UNTEREINHEIT
55	56	RXN02462	VW0124	11932	13749	PREPROTEIN TRANSLOKASE SECA UNTEREINHEIT
57	58	RXN01559	VW0171	7795	5954	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
59	60	RXN00046	VW0119	5363	6058	Signal Erkennung particle GTPase
61	62	RXN01863	VW0206	1172	24	O/C Thioedoxin-ähnliche oxidoreductase
63	64	RXN00833	VW0180	8039	8533	THIOL PEROXIDASE (EC 1.11.1.-)

Chaperones

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Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
65	66	RXN01676	VW0179	12059	11304	THIOL:DISULFIDE AUUSTAUSCH PROTEIN DSBD
67	68	RXN00380	VW0223	836	216	THIOL:DISULFIDE AUUSTAUSCH PROTEIN TLPA
69	70	RXN00937	VW0079	42335	42706	THIOREDOXIN
71	72	RXN02325	VW0047	5527	6393	THIOREDOXIN
73	74	RXN01837	VW0320	7103	7879	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
75	76	RXN01926	VW0284	1	741	PEPTID KETTE RELEASE FACTOR 3
77	78	RXN02002	VW0111	141	518	PEPTID KETTE RELEASE FACTOR 3
79	80	RXN02736	VW0074	13800	14556	PUTATIVES OXPPCYCLE PROTEIN OPCA
81	82	RXS03217				SMALL COLD-SHOCK PROTEIN
83	84	F RXA01917	GR00549	3465	3665	SMALL COLD-SHOCK PROTEIN

Proteins involved in stress responses

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
85	86	RXA02184	GR00641	19628	19248	COLD SHOCK-LIKE PROTEIN CSPC
87	88	RXA00810	GR00218	792	992	SMALL COLD-SHOCK PROTEIN
89	90	RXA01674	GR00467	1878	2771	PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR
91	92	RXA02431	GR00708	2	1192	damage-inducible protein P
93	94	RXA02446	GR00709	11640	11206	OSMOTICALLY INDUCIBLE PROTEIN C
95	96	RXA02861	GR10006	551	1633	probable metallothionein u308aa - Mycobacterium leprae
97	98	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
99	100	RXN00786	VW0321	1680	706	LYTB PROTEIN
101	102	RXS01027	VW0143	5761	6768	DIADENOSINE 5',5"-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
103	104	RXS01528	VW0050	17276	16749	DIADENOSINE 5',5"-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
105	106	RXS01716	VW0319	3259	2774	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
107	108	RXS01835	VW0143	10575	10045	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
109	110	RXS02497	VW0007	15609	16535	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
111	112	RXS02972	VW0319	2763	2353	EXOPOLYPHOSPHATASE (EC 3.6.1.11)

Resistance and tolerance

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
113	114	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
115	116	RXA02201	GR00646	5837	6199	ARSENATE REDUCTASE
117	118	RXA00599	GR00159	1843	1457	ARSENICAL-RESISTANCE PROTEIN ACR3
119	120	RXA00600	GR00159	2940	1843	ARSENICAL-RESISTANCE PROTEIN ACR3
121	122	RXA02200	GR00646	4651	5760	ARSENICAL-RESISTANCE PROTEIN ACR3
123	124	RXA02202	GR00646	6278	6916	ARSENICAL-RESISTANCE PROTEIN ACR3
125	126	RXA02205	GR00646	9871	8993	BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66)
127	128	RXA00900	GR00245	4052	3201	BICYCLOMYCIN RESISTANCE PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
129	130	RXN00901	VW0140	8581	8168	BICYCLOMYCIN RESISTANCE PROTEIN
131	132	F RXA00901	GR00245	4357	3980	BICYCLOMYCIN RESISTANCE PROTEIN
133	134	RXA00289	GR00046	3263	4438	CHLORAMPHENICOL RESISTANCE PROTEIN
135	136	RXN01984	VW0056	1515	1811	CHLORAMPHENICOL RESISTANCE PROTEIN
137	138	F RXA01984	GR00574	282	4	CHLORAMPHENICOL RESISTANCE PROTEIN
139	140	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
141	142	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
143	144	RXA00996	GR00283	1763	1023	DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN DRRA
145	146	RXN00829	VW0180	7950	5611	DAUNORUBICIN RESISTANCE PROTEIN
147	148	F RXA00829	GR00224	2	256	DAUNORUBICIN RESISTANCE PROTEIN
149	150	F RXA00834	GR00225	463	2025	DAUNORUBICIN RESISTANCE PROTEIN
151	152	RXA00995	GR00283	1023	283	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
153	154	RXN00803	VW0009	53858	52629	METHYLENOMYCIN A RESISTANCE PROTEIN
155	156	F RXA00803	GR00214	4560	5162	METHYLENOMYCIN A RESISTANCE PROTEIN
157	158	RXA01407	GR00410	3918	3028	METHYLENOMYCIN A RESISTANCE PROTEIN
159	160	RXA01408	GR00410	4384	4184	METHYLENOMYCIN A RESISTANCE PROTEIN
161	162	RXN01922	VW0020	2031	3182	METHYLENOMYCIN A RESISTANCE PROTEIN
163	164	F RXA01922	GR00552	3	1109	METHYLENOMYCIN A RESISTANCE PROTEIN
165	166	RXA02060	GR00626	1	339	MYCINAMICIN-RESISTANCE PROTEIN MYRA
167	168	RXN01936	VW0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
169	170	F RXA01936	GR00555	9796	8975	NICKEL RESISTANCE PROTEIN
171	172	F RXA01937	GR00555	10246	9821	NICKEL RESISTANCE PROTEIN
173	174	RXN01010	VW0209	3776	4894	QUINOLONE RESISTANCE NORA PROTEIN
175	176	F RXA01010	GR00288	774	4	QUINOLONE RESISTANCE NORA PROTEIN
177	178	RXN03142	VW0136	5754	4612	QUINOLONE RESISTANCE NORA PROTEIN
179	180	F RXA01150	GR00323	3807	2917	QUINOLONE RESISTANCE NORA PROTEIN
181	182	RXN02964	VW0102	7931	6714	QUINOLONE RESISTANCE NORA PROTEIN
183	184	F RXA02116	GR00636	911	6	QUINOLONE RESISTANCE NORA PROTEIN
185	186	RXA00858	GR00233	1680	2147	TELLURIUM RESISTANCE PROTEIN TERC
187	188	RXA02305	GR00663	2921	2070	DAUNOMYCIN C-14 HYDROXYLASE
189	190	RXA00084	GR00013	2367	1543	VIBRIOBACTIN UTILIZATION PROTEIN VIUB
191	192	RXA00843	GR00228	3236	3580	ARSENATE REDUCTASE
193	194	RXA01052	GR00296	3398	3706	MERCURIC REDUCTASE (EC 1.16.1.1)
195	196	RXA01053	GR00296	3772	4191	MERCURIC REDUCTASE (EC 1.16.1.1)
197	198	RXA01054	GR00296	4229	4717	MERCURIC REDUCTASE (EC 1.16.1.1)
199	200	RXN03123	VW0106	808	1245	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
201	202	F RXA00993	GR00282	641	6	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
203	204	RXA01051	GR00296	3298	2690	VANZ PROTEIN, teicoplanin resistance protein
205	206	RXN01873	VW0248	2054	819	Hypothetical Drug Resistance Protein
207	208	F RXA01873	GR00535	855	1946	Hypothetical Drug Resistance Protein
209	210	RXN00034	VW0020	16933	18381	MULTIDRUG RESISTANCE PROTEIN B
211	212	F RXA02273	GR00655	8058	9002	Hypothetical Drug Resistance Protein
213	214	RXN03075	VW0042	2491	3216	Hypothetical Drug Transporter
215	216	F RXA02907	GR10044	1395	2120	Hypothetical Drug Transporter
217	218	RXA00479	GR00119	16290	14101	Hypothetical Drug Transporter
219	220	RXN03124	VW0108	4	963	Hypothetical Drug Transporter
221	222	F RXA01180	GR00336	4	765	Hypothetical Drug Transporter

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	RXA02586	GR00741	10296	10027	Hypothetical Drug Transporter
225	226	RXA02587	GR00741	12343	10253	Hypothetical Drug Transporter
227	228	RXN03042	WV0018	2440	1835	Hypothetical Drug Transporter
229	230	F RXA02893	GR10035	1841	1236	Hypothetical Drug Transporter
231	232	RXA01616	GR00450	1684	203	MULTIDRUG EFFLUX PROTEIN QACB
233	234	RXA01666	GR00463	2307	3683	MULTIDRUG RESISTANCE PROTEIN
235	236	RXA00062	GR00009	13252	11855	MULTIDRUG RESISTANCE PROTEIN B
237	238	RXA00215	GR00032	13834	15294	MULTIDRUG RESISTANCE PROTEIN B
239	240	RXN03064	WV0038	4892	6223	MULTIDRUG RESISTANCE PROTEIN B
241	242	F RXA00565	GR00151	4892	5884	MULTIDRUG RESISTANCE PROTEIN B
243	244	F RXA02878	GR10016	1837	1481	MULTIDRUG RESISTANCE PROTEIN B
245	246	RXA00648	GR00169	2713	1304	MULTIDRUG RESISTANCE PROTEIN B
247	248	RXN01320	WV0082	13146	11500	MULTIDRUG RESISTANCE PROTEIN B
249	250	F RXA01314	GR00382	744	4	MULTIDRUG RESISTANCE PROTEIN B
251	252	F RXA01320	GR00383	1979	1200	MULTIDRUG RESISTANCE PROTEIN B
253	254	RXN02926	WV0082	11497	9866	MULTIDRUG RESISTANCE PROTEIN B
255	256	F RXA01319	GR00383	1197	4	MULTIDRUG RESISTANCE PROTEIN B
257	258	RXA01578	GR00439	1423	29	MULTIDRUG RESISTANCE PROTEIN B
259	260	RXA02087	GR00629	7076	5730	MULTIDRUG RESISTANCE PROTEIN B
261	262	RXA02088	GR00629	8294	7080	MULTIDRUG RESISTANCE PROTEIN B
263	264	RXA00764	GR00204	3284	2169	MULTIDRUG RESISTANCE PROTEIN B
265	266	RXN03125	WV0108	972	1142	BMRU PROTEIN <i>Bacillus subtilis</i> bmrU, multidrug efflux transporter
267	268	RXN01553	WV0135	25201	26520	Hypothetical Drug Transporter
269	270	RXN00535	WV0219	5155	5871	Hypothetical Drug Permease
271	272	RXN00453	WV0076	1173	3521	Hypothetical Drug Resistance Protein
273	274	RXN00932	WV0171	13120	13593	Hypothetical Drug Transporter
275	276	RXN03022	WV0002	65	511	MULTIDRUG RESISTANCE PROTEIN B
277	278	RXN03151	WV0163	489	4	MYCINAMICIN-RESISTANCE PROTEIN MYRA
279	280	RXN02832	WV0358	547	5	LYSOSTAPHIN IMMUNITY FACTOR
281	282	RXN00165	WV0232	3275	1860	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
283	284	RXN01190	WV0169	8992	10338	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
285	286	RXN01102	WV0059	6128	4884	QUINOLONE RESISTANCE NORA PROTEIN
287	288	RXN00788	WV0321	3424	3648	CHLORAMPHENICOL RESISTANCE PROTEIN
289	290	RXN02119	WV0102	11242	9602	A201A-RESISTANCE ATP-BINDING PROTEIN
291	292	RXN01605	WV0137	7124	5610	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
293	294	RXN01091	WV0326	567	4	MAZG PROTEIN
295	296	RXS02979	WV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
297	298	RXS02987	WV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
299	300	RXS03095	WV0057	4056	4424	CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells.</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ24946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Deshydrobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomerase	Keilhauer, C. et al. "Isoleucine synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The <i>Corynebacterium glutamicum</i> accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIIR; cgIIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cgIIIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> ,
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(2):6421 (1990)
X54223		AttB-related site	Ciancio, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(1):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda dacryonephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap; pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	Psl protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding Psl, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of Psl is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glit	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75083, X70584	mttA	5-methyltryptophan resistance	Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75085	recA		Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X77384	recA		Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X78491	aceB	Malate synthase	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Nocardia</i> and evidence for the evolutionary origin of the genus <i>Nocardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X80629	16S rDNA	16S ribosomal RNA	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X81379	dapE	Succinyldiaminopimelate desuccinylase	

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting <i>Arthrobacter aureus</i> C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrijic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xyIB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; fsq/divD; fsz	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the fsz gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicum proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

	glnA	Glutamine synthetase I	
Y13221			Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Coryneophage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?, SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCIC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCIC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

TABLE 4: ALIGNMENT RESULTS

ID #	length_ Genbank Hit (NT)	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
ra00062	1521	GB_HTG2:AC007366	185001	AC007366	Homo sapiens clone NH0501G22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	39,080	5-Jun-99
ra00084	948	GB_PR3:HSU80741	912	U80741	Homo sapiens CAGH44 mRNA, partial cds.	39,264	18-DEC-1997
		GB_PL1:BNDNATRNA	1732	X89901	B. nigra DNA for tRNA like gene.	36,725	6-Feb-97
		GB_PR3:HSU80741	912	U80741	Homo sapiens CAGH44 mRNA, partial cds.	38,957	18-DEC-1997
ra00109	735	GB_GSS9:AQ163721	388	AQ163721	HS_2245_A1_F07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2245 Col=13 Row=K, genomic survey sequence.	45,066	16-OCT-1998
		GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45O18 (D527) RPCI-98 45.O.18 map 41E-41E strain y: cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces.	36,589	13-OCT-1999
		GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45O18 (D527) RPCI-98 45.O.18 map 41E-41E strain y: cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces.	36,589	13-OCT-1999
ra00215	1449	GB_BA1:SC9C7	31360	AL035161	Streptomyces coelicolor cosmid 9C7.	44,444	12-Jan-99
		GB_BA1:SCE94	38532	AL049628	Streptomyces coelicolor cosmid E94.	36,313	12-Apr-99
		GB_BA2:AF110185	20302	AF110185	Burkholderia pseudomallei strain 1026b DbhB (dbhB), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein F (gspF), GspC (gspC), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspI), general secretory pathway protein J (gspJ), general secretory pathway protein K (gspK), general secretory pathway protein L (gspL), general secretory pathway protein M (gspM), and general secretory pathway protein N (gspN) genes, complete cds; and unknown genes.	44,159	2-Aug-99
ra00289	1299	GB_EST6:N80167	384	N80167	za65g02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297458 3', mRNA sequence.	40,420	29-MAR-1996
		GB_STS:G37084	384	G37084	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site.	40,420	30-MAR-1998
		GB_STS:G37084	384	G37084	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site.	40,420	30-MAR-1998
ra00404	2439	GB_BA1:MTCV22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	60,271	17-Jun-98
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	54,256	15-Jan-97
		GB_BA2:AE000165	12003	AE000165	Escherichia coli K-12 MG1655 section 55 of 400 of the complete genome.	54,256	12-Nov-98
ra00479	2313	GB_BA1:SCF43A	35437	AL096837	Streptomyces coelicolor cosmid F43A.	36,245	13-Jul-99
		GB_GSS2:CNS015U4	1036	AL105910	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN14G08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	37,573	26-Jul-99

Table 4 (continued)

GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	36,475	23-Nov-99
GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	40,250	17-Jun-98
GB_BA2:AF079544	817	AF079544	Mycobacterium avium GroESL operon, partial sequence.	Mycobacterium avium	64,439	16-Aug-98
GB_BA1:MTGROEOP	2987	X60350	M.tuberculosis groE gene for KCS and 10-kDa products.	Mycobacterium tuberculosis	62,857	23-Apr-92
na00575						
GB_GSS10:AQ199703	439	AQ199703	RPC111-46O13.TJ RPC11-11 Homo sapiens genomic clone RPC11-11-46O13, genomic survey sequence.	Homo sapiens	42,657	20-Apr-99
GB_PR2:AC002127	144165	AC002127	Human BAC clone RG305H12 from Tq21, complete sequence.	Homo sapiens	37,052	27-MAY-1997
GB_STS:G51234	439	G51234	SHGC-80708 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	42,657	25-Jun-99
GB_BA1:MTCY441	35187	Z80225	Mycobacterium tuberculosis H37Rv complete genome; segment 118/162.	Mycobacterium tuberculosis	56,183	18-Jun-98
GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,217	10-DEC-1996
GB_BA1:BSUB0014	213420	Z99117	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.	Bacillus subtilis	36,553	26-Nov-97
GB_BA2:AF069070	2776	AF069070	Endosymbiont of Onchocerca volvulus catalase gene, complete cds.	endosymbiont of Onchocerca volvulus	55,396	25-Nov-98
GB_BA1:OVCA1	1845	X82176	Onchocerca volvulus endobacterial mRNA for catalase.	Onchocerca volvulus	55,396	26-Nov-98
GB_BA1:SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5.	Streptomyces coelicolor	39,530	11-Jun-99
GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,327	27-Aug-99
GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,327	27-Aug-99
GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	35,119	27-Aug-99
GB_EST36:A1898007	609	A1898007	EST267450 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED31K22, mRNA sequence.	Lycopersicon esculentum	34,323	27-Jul-99
GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds; TrpF (trpF) gene, partial cds; and unknown	Pseudomonas aeruginosa	35,895	23-Jun-98
GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds; TrpF (trpF) gene, partial cds; and unknown	Pseudomonas aeruginosa	41,417	23-Jun-98
GB_IN2:CELH34C03	27748	AF100662	Caenorhabditis elegans cosmid H34C03.	Caenorhabditis elegans	34,152	28-OCT-1998
GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS *** 33 unordered pieces.	Homo sapiens	37,472	24-Jun-99
GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS *** 33 unordered pieces.	Homo sapiens	37,472	24-Jun-99

Table 4 (continued)

rx00810 324	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	34,615	17-Jun-98
rx00829 2463	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	34,615	27-Aug-99
	GB_BA1:ECOUW76	225419	U00039	E. coli chromosomal region from 76.0 to 81.5 minutes.	Escherichia coli	52,997	7-Nov-96
	GB_BA1:SC5C7	41906	AL031515	Streptomyces coelicolor cosmid 5C7.	Streptomyces coelicolor	65,269	7-Sep-98
	GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	37,490	24-MAY-1999
rx00843 468	GB_BA1:STMDRRC	3374	L76359	Streptomyces peuceitii daunorubicin resistance protein (drrC) gene, complete	Streptomyces peuceitii	55,279	24-DEC-1996
	GB_BA1:MTCY9C4	15916	Z77250	Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.	Mycobacterium tuberculosis	40,000	17-Jun-98
rx00858 568	GB_BA1:MTCY9C4	15916	Z77250	Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
rx00886 1269	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	39,602	11-Jun-99
	GB_EST18:N96610	547	N96610	21285 Lambda-PRL1 Arabidopsis thaliana cDNA clone F10G377, mRNA	Arabidopsis thaliana	37,801	5-Jan-98
	GB_EST18:T45493	436	T45493	8756 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133C14T7, mRNA	Arabidopsis thaliana	34,194	4-Aug-98
	GB_BA1:SYCSLLH	132106	D64006	Synechocystis sp. PCC6803 complete genome, 2527, 3138604-3270709.	Synechocystis sp.	37,459	13-Feb-99
	GB_BA1:SCDNAJ	5611	X77458	S. coelicolor dnaK, grpE and dnaJ genes.	Streptomyces coelicolor	49,744	21-Nov-96
	GB_BA1:STMDNAK	4648	L46700	Streptomyces coelicolor (strain A3(2)) dnaK operon encoding molecular chaperones (dnaK, dnaJ), grpE and hspR genes, complete cds's.	Streptomyces coelicolor	49,583	22-Nov-96
	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	38,314	U18997
	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,759	U18997
rx00901 537	GB_BA2:AE000393	10516	AE000393	Escherichia coli K-12 MG1655 section 283 of 400 of the complete genome.	Escherichia coli	38,314	12-Nov-98
	GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	34,857	22-Sep-99
	GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	34,857	22-Sep-99
	GB_HTG3:AC011283	87295	AC011283	Homo sapiens clone MS2016A09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	35,448	07-OCT-1999
rx00981 753	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	Gallus gallus	37,538	28-Sep-99
	GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome 1, complete sequence.	Arabidopsis thaliana	37,600	04-OCT-1999
rx00995 864	GB_GSS1:CNS00RNW542	AL087338	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
	GB_EST29:AI553951	450	AI553951	te54d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090497 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);, mRNA sequence.	Homo sapiens	42,627	13-Apr-99
rx00996 864	GB_PR3:AC003029	139166	AC003029	Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	38,915	17-Sep-98
	GB_BA1:EAY14603	4479	Y14603	Erwinia amylovora srlA, srlE, srlB, srlD, srlM and srlR genes.	Erwinia amylovora	37,694	6-Jan-98
	GB_BA2:AE001001	10730	AE001001	Archaeoglobus fulgidus section 106 of 172 of the complete genome.	Archaeoglobus fulgidus	41,078	15-DEC-1997
	GB_EST30:AV018764	242	AV018764	AV018764 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190006M16, mRNA sequence.	Mus musculus	39,669	28-Aug-99

Table 4 (continued)

GB_GSS3:B24189	377	B24189	F19E16TF IGF Arabidopsis thaliana genomic clone F19E16, genomic survey sequence.	Arabidopsis thaliana	44,385	10-OCT-1997
GB_OV:AF007068	356	AF007068	Coturnix coturnix arylalkylamine N-acetyltransferase mRNA, partial cds.	Coturnix coturnix	46,629	12-Jul-97
GB_EST10:AA166324	514	AA166324	ms50c09.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE:614992 5' similar to SW:NEST_RAT P21263 NESTIN.1; mRNA sequence.	Mus musculus	38,677	19-DEC-1996
GB_EST7:W89968	46	W89968	mfb4g11.1r Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:419108 5' similar to SW:NEST_RAT P21263 NESTIN. [1]; mRNA sequence.	Mus musculus	58,696	12-Sep-96
GB_GSS12:AQ381423	579	AQ381423	RPC111-135F10.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-135F10, genomic survey sequence.	Homo sapiens	37,651	21-MAY-1999
GB_HTG6:AC010901	206121	AC010901	Homo sapiens clone RP11-544J22, WORKING DRAFT SEQUENCE, 1 unordered pieces.	Homo sapiens	36,011	04-DEC-1999
GB_GSS5:AQ746932	837	AQ746932	HS_5538_A1_A11_TTA RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1114 Col=21 Row=A, genomic survey sequence.	Homo sapiens	38,640	19-Jul-99
GB_IN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	39,344	2-Aug-97
GB_IN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	38,780	2-Aug-97
GB_OV:CHKMAFG1	1316	D28601	Chicken novel maf-related gene mafG encoding bZip nuclear protein MafG, promoter region and exon 1.	Gallus gallus	39,205	7-Feb-99
GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***; 26 unordered pieces.	Homo sapiens	32,961	07-DEC-1999
GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***; 26 unordered pieces.	Homo sapiens	38,476	07-DEC-1999
GB_PL1:PHNPNGLP	962	D45425	Pharbitis nil mRNA for Pharbitis nil Germin-like protein precursor, complete cds.	Ipomoea nil	42,925	10-Feb-99
GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	35,794	08-OCT-1999
GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	40,625	08-OCT-1999
GB_RO:MUSMCFTR	6304	M60493	Mouse cystic fibrosis transmembrane conductance regulator (CFTR) mRNA, complete cds.	Mus musculus	37,793	10-Jun-94
GB_BA2:AF031037	1472	AF031037	Neisseria meningitidis chloramphenicol acetyltransferase gene, complete cds.	Neisseria meningitidis	35,014	21-Apr-98
GB_HTG1:PFMAL13PA80518	AL109815	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
GB_HTG1:PFMAL13PA80518	AL109815	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_Q_1, complete sequence.	Homo sapiens	38,195	14-Aug-98
GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_Q_1, complete sequence.	Homo sapiens	36,611	14-Aug-98
GB_HTG3:AC011500_1300851	AC011500	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS***, 246 unordered pieces.	Homo sapiens	36,446	AC011500
GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99

Table 4 (continued)

rx01408 324	GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99
	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	40,778	30-Sep-98
	GB_PR4:AF152365	246546	AF152365	Homo sapiens constitutive fragile region FRA3B sequence.	Homo sapiens	41,234	1-Aug-99
	GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
rx01524 1566	GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540.	Bacillus subtilis	38,201	26-Nov-97
	GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPCI-98 13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.	Drosophila melanogaster	38,302	2-Aug-99
	GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPCI-98 13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.	Drosophila melanogaster	38,302	2-Aug-99
rx01578 1510	GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	37,873	14-Jul-99
	GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	40,220	14-Jul-99
	GB_BA1:AEV13732	6740	Y13732	Alcaligenes eutrophus genes for ureases, ureD1, ureD2, ureA, ureB, and ORF1, ORF2.	Raistonia eutropha	42,960	23-Sep-97
	GB_BA2:AF088857	2908	AF088857	Vogesella indigofera indigoidine biosynthesis regulatory locus, complete Caenorhabditis elegans cosmid M04D8, complete sequence.	Vogesella indigofera	37,626	10-Sep-99
rx01616 1605	GB_IN1:CEM04D8	21552	Z32682	Caenorhabditis elegans cosmid M04D8, complete sequence.	Caenorhabditis elegans	37,237	23-Nov-98
	GB_EST25:AI281910	276	AI281910	qt82d04.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1961767 3', mRNA sequence.	Homo sapiens	38,406	21-DEC-1998
	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	99,933	9-Apr-97
	GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 109 unordered pieces.	Drosophila melanogaster	36,111	23-Aug-99
rx01666 1500	GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 109 unordered pieces.	Drosophila melanogaster	36,111	23-Aug-99
	GB_PL1:AB017159	1859	AB017159	Daucus carota mRNA for citrate synthase, complete cds.	Daucus carota	39,537	01-MAY-1999
	GB_PR1:HUMGNOS4823142	D26607	D26607	Homo sapiens endothelial nitric oxide synthase gene, complete cds.	Homo sapiens	36,419	13-Jul-99
	GB_HTG3:AC011234	154754	AC011234	Homo sapiens clone NH0166D23, *** SEQUENCING IN PROGRESS***, 7 unordered pieces.	Homo sapiens	36,317	04-OCT-1999
rx01673 1359	GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS***, 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
	GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS***, 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
	GB_HTG3:AC009919	134724	AC009919	Homo sapiens clone 115_I_23, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,409	8-Sep-99
	GB_BA1:ECONUC	1676	M84026	E.coli protein p7 (neu C) gene, complete cds.	Escherichia coli	35,189	26-Apr-93

Table 4 (continued)

GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99
GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99
GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/6686 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***. 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999
GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/6686 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***. 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999
GB_PR4:AC005552	167228	AC005552	Homo sapiens chromosome 17, clone hRPK.212 E_8, complete sequence.	Homo sapiens	36,249	26-Nov-98
GB_PR1:HS169C8F	245	Z57239	H.sapiens CpG island DNA genomic MseI fragment, clone 169c8, forward read cpg169c8.ft1a.	Homo sapiens	45,679	18-OCT-1995
GB_BA1:SERATTBXIS	3255	L11597	Saccharopolyspora erythraea excisionase (xis) gene, integrase (int) gene, complete cds's and attB site.	Saccharopolyspora erythraea	36,232	6-Jul-94
GB_EST7:W97557	267	W97557	mf98a09.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:422296 5', mRNA sequence.	Mus musculus	42,969	16-Jul-96
GB_PR3:AC005544	169045	AC005544	Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.	Homo sapiens	35,724	25-Sep-98
GB_PL1:ATF20B18	104738	AL049483	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project).	Arabidopsis thaliana	35,890	24-MAR-1999
GB_PL2:ATT25K17	89904	AL049171	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project).	Arabidopsis thaliana	38,128	27-Aug-99
GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3, *** SEQUENCING IN PROGRESS ***. 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3, *** SEQUENCING IN PROGRESS ***. 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
GB_HTG3:AC008703	213971	AC008703	Homo sapiens chromosome 5 clone CIT978SKB_76P12, *** SEQUENCING IN PROGRESS ***. 54 unordered pieces.	Homo sapiens	34,768	3-Aug-99
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
GB_BA1:BSZ92953	8164	Z92953	B.subtilis yws[A,B,C] genes and rbs[A,C,D,K,R] genes.	glutamicum	38,951	24-Jun-98
GB_EST36:A1878071	593	A1878071	fc57a12.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0	Bacillus subtilis	36,774	21-Jul-99
			.. mRNA sequence.	Danio rerio		

Table 4 (continued)

GB_EST37:A1958166	641	A1958166	fc91f01.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0 ; mRNA sequence.	Danio rerio	36,774	20-Aug-99
GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	38,648	23-Nov-99
GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS ***; 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS ***; 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:50010 5'; Homo sapiens mRNA sequence.	Homo sapiens	38,267	29-Jun-95
GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:50010 5'; Homo sapiens mRNA sequence.	Homo sapiens	36,552	29-Jun-95
GB_IN1:CELC41A3	37149	U41541	Caenorhabditis elegans cosmid C41A3.	Caenorhabditis elegans	41,678	08-DEC-1995
GB_EST33:AV080151	236	AV080151	AV080151 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2210413B04, mRNA sequence.	Mus musculus	43,348	25-Jun-99
GB_GSS5:AQ766877	545	AQ766877	HS_2017_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2017 Co1=16 Row=D, genomic survey sequence.	Homo sapiens	35,568	28-Jul-99
GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
GB_IN1:BRPTUBBA	4571	M36380	B.pahangi beta-tubulin gene, complete cds.	Brugia pahangi	37,703	26-Apr-93
GB_RO:MU5PAFR	1140	D50872	Mouse gene for platelet activating factor receptor, complete cds.	Mus musculus	38,420	10-Feb-99
GB_PR3:HUMARL1A	1008	L28997	Homo sapiens ARL1 mRNA, complete cds.	Homo sapiens	42,188	13-Jan-95
GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	42,000	27-Aug-99
GB_EST4:H35255	407	H35255	EST111890 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNC003, mRNA sequence.	Rattus sp.	39,098	2-Apr-98
GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	39,456	23-Nov-99
GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	39,456	23-Nov-99
GB_BA2:AF036166	895	AF036166	Xanthomonas campestris organic hydroperoxide resistance protein (ohr) gene, complete cds.	Xanthomonas campestris	49,369	19-MAY-1998
GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	35,417	28-DEC-1995
GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	37,172	28-DEC-1995
GB_BA2:DPU93358	1267	U93358	Deinococcus proteolyticus 40 kDa heat shock chaperone protein (dnaJ) gene, complete cds.	Deinococcus proteolyticus	42,115	17-Jan-98
GB_EST30:A1658096	343	A1658096	fc14c09.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAB PROTEIN HOMOLOG 2. ; mRNA sequence.	Danio rerio	52,059	06-MAY-1999
GB_EST37:A1959242	545	A1959242	fd25h11.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAB PROTEIN HOMOLOG 2. ; mRNA sequence.	Danio rerio	45,438	20-Aug-99

Table 4 (continued)

rx02542 777	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	99,000	08-OCT-1997 (Rel. 52, Created).
rx02543 1977	GB_EST24:Z82017	396	Z82017	SSZ82017 Porcine small intestine cDNA library Sus scrofa cDNA clone c12c06 5' similar to eukaryotic initiation factor 4 gamma, mRNA sequence.	Sus scrofa	37,067	30-Apr-99
	GB_OM:CATERYTHRO881		L10606	Cat erythropoietin mRNA, 3' end.	Felis catus	39,409	14-OCT-1993
	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	97,306	08-OCT-1997 (Rel. 52, Created)
rx02586 393	GB_BA1:MPHSP70	2179	X59437	M.paratuberculosis gene for 70 kD heat shock protein.	Mycobacterium avium subsp. paratuberculosis	73,404	23-Apr-92
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	72,028	17-Jun-98
	GB_IN2:AC006472	156362	AC006472	Drosophila melanogaster, chromosome 2R, region 45E1-46A2, BAC clone BACR48G21, complete sequence.	Drosophila melanogaster	37,958	30-Jan-99
	GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPC198-2613, *** SEQUENCING IN PROGRESS ***; 55 unordered pieces.	Drosophila melanogaster	37,333	16-OCT-1999
	GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPC198-2613, *** SEQUENCING IN PROGRESS ***; 55 unordered pieces.	Drosophila melanogaster	37,333	16-OCT-1999
rx02587 2214	GB_BA1:MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622.	Mycobacterium leprae	39,848	24-Jun-97
	GB_RO:AF074879	3316	AF074879	Rattus norvegicus testis-specific protein TSPY gene, complete cds.	Rattus norvegicus	35,830	6-Jul-99
	GB_RO:RNJ001380	2641	AJ001380	Rattus norvegicus Tspy partial genomic sequence, exons 1-6.	Rattus norvegicus	37,702	29-Jun-98
	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	37,888	27-Aug-99
	GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	36,420	4-Feb-00
rx03217 331	GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	35,962	4-Feb-00

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

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Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* 10 (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & 15 Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome 25 Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

30 *In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, *mutHLS*, *mutD*, *mutT*, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vector into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by
20 sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in
25 Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

- 91 -

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

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Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

30

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall yield, production, and/or efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. 20 Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

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cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

EXAMPLE 11: Cloning of a *Corynebacterium glutamicum* Gene Involved in Lincomycin Resistance Using a Reporter Gene Approach

A. Identification of the Gene Encoding the LMRB Protein

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Plasmid pSL130 was constructed by ligation of the *aceB* promoter region (paceB) of *C. glutamicum* (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) into the polylinker of the lac operon fusion vector pRS415, which lacks a promoter (Simon, R.W. *et al.* (1987) *Gene* 53: 85-96). Plasmid pSL145 was constructed by
5 ligating the resulting paceB-lac region into the *E. coli* cloning vector pACYC184. *E. coli* DH5 α F' was transformed with pSL145 and the resulting strain was used as a host for screening of a genomic *C. glutamicum* library (in pSL109).

Transformants were screened by growth on agar medium containing 5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside (X-Gal). A white colony, containing DNA
10 influencing lacZ expression, was selected for further analysis. This clone was found to contain a 4 kB fragment from the gene library. Subclones were constructed in pSL109 and a subclone which retained the white phenotype on X-Gal plates was identified. This subclone was found to contain a 2.6 kB BamH1-XhoI fragment (plasmid pSL149-5). The fragment was sequenced and identified as a membrane protein-encoding gene
15 (LMRB gene).

The 1442 nucleotides of the coding sequence of the LMRB gene encode a polypeptide of 481 amino acid residues with a high percentage of hydrophobic amino acids. A Genbank search determined that the LMRB protein is 40% identical to the protein product of the *lmrB* gene from *Bacillus subtilis* (Genbank Accession AL009126,
20 TREMBL Accession P94422), as determined using a CLUSTAL W analysis (using standard parameters).

The LMRN protein contains a sequence pattern: 158-A-P-A-L-G-P-T-L-S-G-167 (SEQ ID NO:301), which resembles the known multi-drug-resistance-protein consensus motif G-X-X-X-G-P-X-X-G-G (SEQ ID NO:302) (Paulsen, I.T., and Skurray, R.A.
25 (1993) *Gene* 124: 1-11). Therefore, the LMRB protein was classified as a drug resistance protein.

B. In vivo Analysis of lmrB Function

The *lmrB* gene was overexpressed in *C. glutamicum* ASO19E12 (Kim, H.J. *et al.*
30 (1997) *J. Microbiol. Biotechnol.* 7: 287-292) using the plasmid pSL149-5, described above.

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Disruption of the LMRB gene was accomplished by use of the vector pSL18-lmrB. This vector was constructed as follows: an internal fragment of the LMRB gene was amplified by PCR under standard conditions using primers 5'-

CTCCAGGATTGCTCCGAAGG-3' (SEQ ID NO:303) and 5'-

- 5 CACAGTGGTTGACCACTGGC-3' (SEQ ID NO:304). The resulting PCR product was treated with T7 DNA polymerase and T7 polynucleotide kinase, and was cloned into the SmaI site of plasmid pSL18 (Kim, Y.H. and H.-S. Lee (1996) *J. Microbiol. Biotechnol.* 6: 315-320). The disruption of the LMRB gene in *C. glutamicum* ASO19E12 was performed by conjugation, as previously described (Schwarzer and
10 Puhler (1991) *Bio/Technology* 9:84-87).

- C. glutamicum* cells transformed with pSL149-5 displayed similar resistances as untransformed cells against erythromycin, penicillin G, tetracycline, chloramphenicol, spectinomycin, nalidixic acid, gentamycin, streptomycin, ethidium bromide, carbonyl cyanide m-chlorophenylhydrazone (CCCP), and sodium dodecyl sulfate. Significant
15 differences were observed, however, in the resistance of transformed and untransformed cells to lincomycin.

- LMRB-overexpressing *C. glutamicum* cells were found to be able to grow in the presence of 20 µg/ml lincomycin. In contrast, cells which do not overexpress LMRB (or cells carrying a LMRB disruption) were not able to grow on agar media containing 5
20 µg/ml lincomycin. This effect was clearly visible in liquid culture. LMRB overexpression led to a 9-fold increased resistance (compared to wild-type) against lincomycin and LMRB disruption resulted in a decreased resistance (28% of wild-type) to this antibiotic.

25 **Example 12: Analysis of the Gene Sequences of the Invention**

- The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*
30 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100,

wordlength = 12 to obtain nucleotide sequences homologous to SRT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SRT protein molecules of the invention. To obtain gapped alignments
5 for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

10 Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN
15 program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be
20 accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a
25 length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention
30 were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the

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top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP
5 program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of
10 the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment
15 homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 13: Construction and Operation of DNA Microarrays

20 The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.*
25 (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label
30 may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic

acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C.*

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glutamicum or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 14: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and

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include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a stress, resistance, or tolerance gene, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said stress, resistance, or tolerance gene is selected from the group consisting of nucleic acid molecules involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

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a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides
5 of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 10 8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous
15 polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
- 20 12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
- 25 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
- 30 16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

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and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

- 5 17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated stress, resistance, or tolerance polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 10 19. The protein of claim 18, wherein said stress, resistance, or tolerance polypeptide is selected from the group consisting of proteins involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.
- 15 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 20 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
- 25 by any of the F-designated genes set forth in Table 1.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 30 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID

NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujikense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group
5 consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
- 10 32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
15 tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
- 20 35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more SEQ ID NOs 1 through 304 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby
25 diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
- 30 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the

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Sequence Listing , wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing .

- 5 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
 <120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
 RESISTANCE AND TOLERANCE PROTEINS
 <130> BGI-124CPPC

<140>

<141>

<160> 304

<210> 1

<211> 1566

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1543)

<223> RXA01524

<400> 1

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                                         Met Asp Ser Gln Ile
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aat act cag acc tct ccg gca gct gcg aag ctg cct agg gag gtc gtt 163
Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu Pro Arg Glu Val Val
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Val Val Leu Ser Ile Leu Val Val Ser Ala Met Ile Met Ile Leu Asn
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gaa acc att ctg tcg gtt gcg ttg cct tcc atc atg gaa gat ttc tcc 259
Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile Met Glu Asp Phe Ser
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Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr Gly Phe Met Leu Thr
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Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu Leu Asp Arg Phe Ser
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act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg 403
Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
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ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt 451
Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
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Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr

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tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met 170 175 180			643
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gtg gtc atg cac gtt gtg ttc agc atc ggc atg tgt ttg atg atg acc 1267
 Val Val Met His Val Val Phe Ser Ile Gly Met Cys Leu Met Met Thr
 375 380 385

cct ctc atg acc acc gct ctc ggc gcc ctt ccg aag cac ctc tat ggt 1315
 Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro Lys His Leu Tyr Gly
 390 395 400 405

cac ggc tcc gca att ttg aac acg ttc caa cag ctc gca ggc gca gcc 1363
 His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln Leu Ala Gly Ala Ala
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 425 430 435

gcg tct tcg gga tct gcg cat gct gaa gct gtt gcc gct ggt acc aag 1459
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<213> Corynebacterium glutamicum

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 20 25 30

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 35 40 45

Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
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Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
 65 70 75 80

Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
 85 90 95

Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
 100 105 110

Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
 115 120 125

Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
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Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
 145 150 155 160

Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
 165 170 175

Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile
 180 185 190

Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
 195 200 205

Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
 210 215 220

Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
 225 230 235 240

Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
 245 250 255

Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
 260 265 270

Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
 275 280 285

Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
 290 295 300

Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
 305 310 315 320

Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
 325 330 335

Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
 340 345 350

Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
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Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
 370 375 380

Cys Leu Met Met Thr Pro Leu Met Thr Thr Ala L u Gly Ala Leu Pro
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 Lys His Leu Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln
 405 410 415
 Leu Ala Gly Ala Ala Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe
 420 425 430
 Gly Thr Ser Ile Ala Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val
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 <223> RXA00497

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 gaa gca gag acc acc acc gct tcc ggc ctg gtc att cca gat tcc gct 153
 Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp Ser Ala
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 aag gaa aag cca caa gag gca acc gtt atc gca gtt ggc cca ggc cgc 201
 Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro Gly Arg
 35 40 45 50
 ttc gat gac aag ggt aac cgc atc cca ctg gac atc aag gaa gat gac 249
 Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu Asp Asp
 55 60 65
 gtt gtg atc ttc tcc cgt tac ggc ggc acc gag atc aag ttc ggt ggc 297
 Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe Gly Gly
 70 75 80

gtg gag tac ttg ctt ctc tcc gct cgt gac atc ctc gca atc gtc gag 345
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 35 40 45

Gly Arg Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu
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Asp Asp Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe
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 Met Ala Lys Leu Ile
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gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
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Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val	
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Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val	
40 45 50	
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Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly	
55 60 65	
gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt	355
Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly	
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gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa	403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu	
90 95 100	
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Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	
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Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	
185 190 195	
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Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu	
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gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca	787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro	
215 220 225	
gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg	835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu	
230 235 240 245	

ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt	883
Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val	
250 255 260	
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Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro	
265 270 275	
tac ttc ggt gac cga cgc aag gcg ttc atg gat gac ctg gct att gtc	979
Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val	
280 285 290	
acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa	1027
Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu	
295 300 305	
gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag	1075
Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys	
310 315 320 325	
gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa	1123
Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu	
330 335 340	
gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc	1171
Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr	
345 350 355	
tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt	1219
Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly	
360 365 370	
att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac	1267
Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp	
375 380 385	
cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca	1315
Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala	
390 395 400 405	
caa gaa ggc gtt atc gct ggt ggc ggt tcc gct ttg gtt cag atc gct	1363
Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala Leu Val Gln Ile Ala	
410 415 420	
gag act ctg aag gct tac gcc gaa gag ttc gaa ggc gac cag aag gtc	1411
Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu Gly Asp Gln Lys Val	
425 430 435	
ggc gtt cgc gca ctg gct act gct ttg ggc aag cca gcg tac tgg atc	1459
Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys Pro Ala Tyr Trp Ile	
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gcc tcc aac gca ggt ctt gac ggc tct gtt gtt gtt gca cgc act gct	1507
Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val Val Ala Arg Thr Ala	
455 460 465	
gct ctg cca aac ggc gag ggc ttc aac gct gca act ttg gaa tac gga	1555

Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala Thr Leu Glu Tyr Gly
 470 475 480 485

aac ctg atc aac gac ggt gtc atc gac cca gtc aag gtc acc cat tcc 1603
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 490 495 500

gca gta gtg aat gca acc tct gtt gca cgc atg gtt ctg acc act gag 1651
 Ala Val Val Asn Ala Thr Ser Val Ala Arg Met Val Leu Thr Thr Glu
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gct tct gtt gtt gag aag cct gca gaa gaa gca gcc gat gca cat gca 1699
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 Gly His His His His
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 35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
 50 55 60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
 65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
 85 90 95

Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110

Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
 115 120 125

Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
 130 135 140

Asn Val Ala Thr Val Ser Arg Asp Glu Val Val Gly Glu Ile Val
 145 150 155 160

Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu

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Phe	Asp	Lys	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Asp	Asn	Asp	Thr															
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225					230					235					240															
Ser	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro															
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Gly	Asp	Gln	Lys	Val	Gly	Val	Arg	Ala	Leu	Ala	Thr	Ala	Leu	Gly	Lys															
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Pro	Ala	Tyr	Trp	Ile	Ala	Ser	Asn	Ala	Gly	Leu	Asp	Gly	Ser	Val	Val															
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Val	Ala	Arg	Thr	Ala	Ala	Leu	Pro	Asn	Gly	Glu	Gly	Phe	Asn	Ala	Ala															

465	470	475	480
Thr Leu Glu Tyr	Gly Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val		
	485	490	495
Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala Arg Met			
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Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala			
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Ala Asp Ala His Ala Gly His His His His			
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<222> (101)..(1339)

<223> FRXA00498

<400> 7

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                                         Met Ala Lys Leu Ile
                                         1 5

gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala
                        10 15 20

ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg 211
Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val
                        25 30 35

gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc 259
Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val
                        40 45 50

acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt 307
Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly
                        55 60 65

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Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly
                        70 75 80 85

gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa 403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu
                        90 95 100

ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag 451

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Gly Leu Arg	Asn Val Ala Ala Gly	Ala Asn Pro Met Glu	Leu Asn Lys	
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Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg	120	125	130	
gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt				547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val	135	140	145	
tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa				595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu	150	155	160	165
aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc				643
Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	170	175	180	
gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac				691
Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	185	190	195	
ctt tcc cct tat ttc atc aac gac aac gac act cag cag gct gtc ctg				739
Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu	200	205	210	
gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca				787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro	215	220	225	
gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg				835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu	230	235	240	245
ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt				883
Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val	250	255	260	
gtg aac tcc atc cgc aag acc atc aag gtc gtt gca gtg aag tcc cct				931
Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro	265	270	275	
tac ttc ggt gac cga cgc aag gcg ttc atg gat gac ctg gct att gtc				979
Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val	280	285	290	
acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa				1027
Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu	295	300	305	
gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag				1075
Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys	310	315	320	325
gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa				1123
Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu				

330	335	340	
gca cgt cgc ggc cag atc cgt cgc	gaa atc gcc aac acc gat tcc acc	1171	
Ala Arg Arg Gly Gln Ile Arg Arg	Glu Ile Ala Asn Thr Asp Ser Thr		
345	350 355		
tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt	1219		
Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly			
360	365 370		
att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac	1267		
Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp			
375	380 385		
cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca	1315		
Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala			
390	395 400 405		
caa gaa ggc gtt atc gct ggt ggc	1339		
Gln Glu Gly Val Ile Ala Gly Gly			
410			

<210> 8

<211> 413

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

Met Ala Lys Leu Ile Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu	
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Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro	
20 25 30	
Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val	
35 40 45	
Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro	
50 55 60	
Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr	
65 70 75 80	
Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln	
85 90 95	
Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro	
100 105 110	
Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu	
115 120 125	
Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala	
130 135 140	
Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val	

145	150	155	160
Ala Ala Ala Met	Glu Lys Val Gly Lys	Asp Gly Val Val Thr	Val Glu
	165	170	175
Glu Ser Gln Ser	Ile Glu Thr Ala Leu	Glu Val Thr Glu Gly	Ile Ser
	180	185	190
Phe Asp Lys Gly Tyr	Leu Ser Pro Tyr Phe	Ile Asn Asp Asn Asp	Thr
	195	200	205
Gln Gln Ala Val	Leu Asp Asn Pro Ala Val	Leu Leu Val Arg Asn	Lys
	210	215	220
Ile Ser Ser Leu Pro	Asp Phe Leu Pro Leu	Leu Glu Lys Val Val	Glu
	225	230	235
Ser Asn Arg Pro	Leu Leu Ile Ile Ala	Glu Asp Val Glu Gly	Glu Pro
	245	250	255
Leu Gln Thr Leu Val	Val Asn Ser Ile Arg Lys	Thr Ile Lys Val Val	
	260	265	270
Ala Val Lys Ser Pro	Tyr Phe Gly Asp Arg Arg	Lys Ala Phe Met Asp	
	275	280	285
Asp Leu Ala Ile Val	Thr Lys Ala Thr Val Val	Asp Pro Glu Val Gly	
	290	295	300
Ile Asn Leu Asn Glu	Ala Gly Glu Glu Val	Phe Gly Thr Ala Arg	Arg
	305	310	315
Ile Thr Val Ser Lys	Asp Glu Thr Ile Ile Val	Asp Gly Ala Gly Ser	
	325	330	335
Ala Glu Asp Val Glu	Ala Arg Arg Gly Gln Ile	Arg Arg Glu Ile Ala	
	340	345	350
Asn Thr Asp Ser Thr	Trp Asp Arg Glu Lys Ala	Glu Glu Arg Leu Ala	
	355	360	365
Lys Leu Ser Gly Gly	Ile Ala Val Ile Arg Val	Gly Ala Ala Thr Glu	
	370	375	380
Thr Glu Val Asn Asp	Arg Lys Leu Arg Val	Glu Asp Ala Ile Asn	Ala
	385	390	395
Ala Arg Ala Ala Ala	Gln Glu Gly Val Ile Ala	Gly Gly	
	405	410	

<210> 9

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01217

<400> 9

gcgctgcctg cgaagactcg accaagacat tcgagtcggt cgcgggcatt ttttattttc 60

gcggccgagt gtccaccttc atccatgagg agaaatcact atg gca aag tac caa 115
 Met Ala Lys Tyr Gln
 1 5

acc att gag gct gct gtc cgc tct gag ttc ggc aag ggc tct gca cgt 163
 Thr Ile, Glu Ala Ala Val Arg Ser Glu Phe Gly Lys Gly Ser Ala Arg
 10 15 20

cgt gca cgc gtt gct ggc cag atc cct gct gtt gtt tac ggc gca gat 211
 Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val Val Tyr Gly Ala Asp
 25 30 35

gtt gag tcc aac ctg cac gtc acc atc gac cac cgc acc ttc gct gcg 259
 Val Glu Ser Asn Leu His Val Thr Ile Asp His Arg Thr Phe Ala Ala
 40 45 50

ctg gtt cgc cag gaa ggc gta aac gct gtt ctt gag ctc gac atc gag 307
 Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu Glu Leu Asp Ile Glu
 55 60 65

ggc cag aag cag ctc acc atg atc aag cac atc gac cag aac gtg ctg 355
 Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile Asp Gln Asn Val Leu
 70 75 80 85

acc ttc cac atc gac cac ttg gac ctg ctt gcc att aag cgc ggc gaa 403
 Thr Phe His Ile Asp His Leu Asp Leu Leu Ala Ile Lys Arg Gly Glu
 90 95 100

aag gtt gag gtt gac gtt cca gtt atc gtc gag ggc gag cca gct cca 451
 Lys Val Glu Val Asp Val Pro Val Ile Val Glu Gly Glu Pro Ala Pro
 105 110 115

ggc acc atg tgg gtt cag gat gct gac acc atc aag gtt gag gct gac 499
 Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile Lys Val Glu Ala Asp
 120 125 130

gtt ctg tcc atc cct gaa gag ttc acc gtt tcc atc gaa ggc ctt gag 547
 Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser Ile Glu Gly Leu Glu
 135 140 145

ctc ggc gca cag atc acc gca gct gac atc aag ctc gag ggc gac acc 595
 Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys Leu Glu Gly Asp Thr
 150 155 160 165

acc ctg gtt gag gat cct gag acc ctc atc gtc aac atc gtt ctc cca 643
 Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val Asn Ile Val Leu Pro
 170 175 180

gct gtc gag gaa gaa gac acc gaa gag gac gaa gca gct gaa gaa gca 691
 Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu Ala Ala Glu Glu Ala

185

190

195

gct act gag taagcttttt tagatagctt tat

723

Ala Thr Glu

200

<210> 10

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

Met Ala Lys Tyr Gln Thr Ile Glu Ala Ala Val Arg Ser Glu Phe Gly
1 5 10 15Lys Gly Ser Ala Arg Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val
20 25 30Val Tyr Gly Ala Asp Val Glu Ser Asn Leu His Val Thr Ile Asp His
35 40 45Arg Thr Phe Ala Ala Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu
50 55 60Glu Leu Asp Ile Glu Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile
65 70 75 80Asp Gln Asn Val Leu Thr Phe His Ile Asp His Leu Asp Leu Leu Ala
85 90 95Ile Lys Arg Gly Glu Lys Val Glu Val Asp Val Pro Val Ile Val Glu
100 105 110Gly Glu Pro Ala Pro Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile
115 120 125Lys Val Glu Ala Asp Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser
130 135 140Ile Glu Gly Leu Glu Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys
145 150 155 160Leu Glu Gly Asp Thr Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val
165 170 175Asn Ile Val Leu Pro Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu
180 185 190Ala Ala Glu Glu Ala Ala Thr Glu
195 200

<210> 11

<211> 1603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (33)..(1580)

<223> RXA00605

<400> 11

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Met Ser Glu Lys Ser Ala Ala	
1 5	
gac cag atc gta gat cgc gga atg cgt cca aag ctt tct gga aac act	101
Asp Gln Ile Val Asp Arg Gly Met Arg Pro Lys Leu Ser Gly Asn Thr	
10 15 20	
acc cgc cac aac gga gca cca gtt cca tct gag aac atc tcc gca acc	149
Thr Arg His Asn Gly Ala Pro Val Pro Ser Glu Asn Ile Ser Ala Thr	
25 30 35	
gca ggc cca cag ggt cca aac gtt ctc aat gac att cac ctc att gaa	197
Ala Gly Pro Gln Gly Pro Asn Val Leu Asn Asp Ile His Leu Ile Glu	
40 45 50 55	
aag ctc gca cac ttt aac cgc gag aac gtt cca gag cgt atc cct cac	245
Lys Leu Ala His Phe Asn Arg Glu Asn Val Pro Glu Arg Ile Pro His	
60 65 70	
gca aag ggc cac ggc gct ttc ggt gag ctg cac atc acc gag gac gta	293
Ala Lys Gly His Gly Ala Phe Gly Glu Leu His Ile Thr Glu Asp Val	
75 80 85	
tcc gaa tac acc aag gca gac ctg ttc cag cct ggt aag gtc acc ccg	341
Ser Glu Tyr Thr Lys Ala Asp Leu Phe Gln Pro Gly Lys Val Thr Pro	
90 95 100	
ctg gct gtt cgc ttc tct act gtt gct ggt gag cag ggc tcc cca gat	389
Leu Ala Val Arg Phe Ser Thr Val Ala Gly Glu Gln Gly Ser Pro Asp	
105 110 115	
acc tgg cgc gac gtc cac ggc ttc gct ctt cgc ttc tac acc gaa gag	437
Thr Trp Arg Asp Val His Gly Phe Ala Leu Arg Phe Tyr Thr Glu Glu	
120 125 130 135	
ggc aac tac gac atc gtg ggt aac aac acc cca acc ttc ttc ctt cgt	485
Gly Asn Tyr Asp Ile Val Gly Asn Asn Thr Pro Thr Phe Phe Leu Arg	
140 145 150	
gac ggc atg aag ttc ccg gac ttc atc cac tca cag aag cgt ctc aac	533
Asp Gly Met Lys Phe Pro Asp Phe Ile His Ser Gln Lys Arg Leu Asn	
155 160 165	
aag aac ggt ctg cgc gat gca gac atg cag tgg gat ttc tgg acc cgc	581
Lys Asn Gly Leu Arg Asp Ala Asp Met Gln Trp Asp Phe Trp Thr Arg	
170 175 180	
gca cct gaa tct gca cac cag gtg acc tac ctg atg ggt gac cgc ggt	629
Ala Pro Glu Ser Ala His Gln Val Thr Tyr Leu Met Gly Asp Arg Gly	

185	190	195	
acc cct aag acc tcc cgc cac cag gac ggc ttc ggc tcc cac acc ttc Thr Pro Lys Thr Ser Arg His Gln Asp Gly Phe Gly Ser His Thr Phe 200 205 210 215			677
cag tgg atc aac gct gaa ggt aag cca gtt tgg gtt aag tac cac ttc Gln Trp Ile Asn Ala Glu Gly Lys Pro Val Trp Val Lys Tyr His Phe 220 225 230			725
aag acc cgc cag ggc tgg gat tgc ttc acc gat gca gaa gca gca aag Lys Thr Arg Gln Gly Trp Asp Cys Phe Thr Asp Ala Glu Ala Ala Lys 235 240 245			773
gtt gca ggc gag aac gct gac tac cag cgc gaa gac ctc tac aac gct Val Ala Gly Glu Asn Ala Asp Tyr Gln Arg Glu Asp Leu Tyr Asn Ala 250 255 260			821
att gaa aac ggc gac ttc cca atc tgg gac gtc aag gtt cag atc atg Ile Glu Asn Gly Asp Phe Pro Ile Trp Asp Val Lys Val Gln Ile Met 265 270 275			869
cct ttc gag gat gca gag aac tac cgc tgg aac cca ttc gac ctg acc Pro Phe Glu Asp Ala Glu Asn Tyr Arg Trp Asn Pro Phe Asp Leu Thr 280 285 290 295			917
aag acc tgg tcc cag aag gat tac cca ctg atc cca gtc ggt tac ttc Lys Thr Trp Ser Gln Lys Asp Tyr Pro Leu Ile Pro Val Gly Tyr Phe 300 305 310			965
atc ctg aac cgc aac cca cgc aac ttc ttc gct cag atc gag cag ctt Ile Leu Asn Arg Asn Pro Arg Asn Phe Phe Ala Gln Ile Glu Gln Leu 315 320 325			1013
gca ctg gat cca ggc aac atc gtt cct ggc gtc ggc ctg tcc cca gac Ala Leu Asp Pro Gly Asn Ile Val Pro Gly Val Gly Leu Ser Pro Asp 330 335 340			1061
cgc atg ctc cag gca cgt atc ttc gca tac gct gac cag cag cgt tac Arg Met Leu Gln Ala Arg Ile Phe Ala Tyr Ala Asp Gln Gln Arg Tyr 345 350 355			1109
cgc atc ggc gct aac tac cgc gac ctg cca gtg aac cgt cca atc aac Arg Ile Gly Ala Asn Tyr Arg Asp Leu Pro Val Asn Arg Pro Ile Asn 360 365 370 375			1157
gag gtc aac acc tac agc cgc gaa ggt tcc atg cag tac atc ttc gac Glu Val Asn Thr Tyr Ser Arg Glu Gly Ser Met Gln Tyr Ile Phe Asp 380 385 390			1205
gct gag ggc gag cct tcc tac agc cct aac cgc tac gac aag ggc gca Ala Glu Gly Glu Pro Ser Tyr Ser Pro Asn Arg Tyr Asp Lys Gly Ala 395 400 405			1253
ggc tac ctg gat aac ggt acg gat tcc tcc tcc aac cac acc tcc tac Gly Tyr Leu Asp Asn Gly Thr Asp Ser Ser Ser Asn His Thr Ser Tyr 410 415 420			1301

ggc cag gct gat gac atc tac gtc aac cca gac cca cac ggc acc gac 1349
 Gly Gln Ala Asp Asp Ile Tyr Val Asn Pro Asp Pro His Gly Thr Asp
 425 430 435
 ctg gtt cgt gct gct tac gtc aag cac cag gat gat gac gac ttc atc 1397
 Leu Val Arg Ala Ala Tyr Val Lys His Gln Asp Asp Asp Asp Phe Ile
 440 445 450 455
 cag cca ggc atc cta tac cgc gag gtc ctg gat gag ggc gag aag gag 1445
 Gln Pro Gly Ile Leu Tyr Arg Glu Val Leu Asp Glu Gly Glu Lys Glu
 460 465 470
 cga ttg gca gac aac atc tcc aac gca atg cag ggc atc tct gag gca 1493
 Arg Leu Ala Asp Asn Ile Ser Asn Ala Met Gln Gly Ile Ser Glu Ala
 475 480 485
 acc gag cca cgc gtc tac gac tac tgg aac aac gtt gat gag aac ctc 1541
 Thr Glu Pro Arg Val Tyr Asp Tyr Trp Asn Asn Val Asp Glu Asn Leu
 490 495 500
 ggc gct cgc gtc aag gag ctt tac ctc cag aag aag gct taagtccttc 1590
 Gly Ala Arg Val Lys Glu Leu Tyr Leu Gln Lys Lys Ala
 505 510 515
 tgatttaaaa tga 1603

<210> 12

<211> 516

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 12

Met Ser Glu Lys Ser Ala Ala Asp Gln Ile Val Asp Arg Gly Met Arg
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Pro Lys Leu Ser Gly Asn Thr Thr Arg His Asn Gly Ala Pro Val Pro
 20 25 30

Ser Glu Asn Ile Ser Ala Thr Ala Gly Pro Gln Gly Pro Asn Val Leu
 35 40 45

Asn Asp Ile His Leu Ile Glu Lys Leu Ala His Phe Asn Arg Glu Asn
 50 55 60

Val Pro Glu Arg Ile Pro His Ala Lys Gly His Gly Ala Phe Gly Glu
 65 70 75 80

Leu His Ile Thr Glu Asp Val Ser Glu Tyr Thr Lys Ala Asp Leu Phe
 85 90 95

Gln Pro Gly Lys Val Thr Pro Leu Ala Val Arg Phe Ser Thr Val Ala
 100 105 110

Gly Glu Gln Gly Ser Pro Asp Thr Trp Arg Asp Val His Gly Phe Ala
 115 120 125

Leu Arg Phe Tyr Thr Glu Glu Gly Asn Tyr Asp Ile Val Gly Asn Asn
 130 135 140
 Thr Pro Thr Ph Phe Leu Arg Asp Gly Met Lys Phe Pro Asp Phe Ile
 145 150 155 160
 His Ser Gln Lys Arg Leu Asn Lys Asn Gly Leu Arg Asp Ala Asp Met
 165 170 175
 Gln Trp Asp Phe Trp Thr Arg Ala Pro Glu Ser Ala His Gln Val Thr
 180 185 190
 Tyr Leu Met Gly Asp Arg Gly Thr Pro Lys Thr Ser Arg His Gln Asp
 195 200 205
 Gly Phe Gly Ser His Thr Phe Gln Trp Ile Asn Ala Glu Gly Lys Pro
 210 215 220
 Val Trp Val Lys Tyr His Phe Lys Thr Arg Gln Gly Trp Asp Cys Phe
 225 230 235 240
 Thr Asp Ala Glu Ala Ala Lys Val Ala Gly Glu Asn Ala Asp Tyr Gln
 245 250 255
 Arg Glu Asp Leu Tyr Asn Ala Ile Glu Asn Gly Asp Phe Pro Ile Trp
 260 265 270
 Asp Val Lys Val Gln Ile Met Pro Phe Glu Asp Ala Glu Asn Tyr Arg
 275 280 285
 Trp Asn Pro Phe Asp Leu Thr Lys Thr Trp Ser Gln Lys Asp Tyr Pro
 290 295 300
 Leu Ile Pro Val Gly Tyr Phe Ile Leu Asn Arg Asn Pro Arg Asn Phe
 305 310 315 320
 Phe Ala Gln Ile Glu Gln Leu Ala Leu Asp Pro Gly Asn Ile Val Pro
 325 330 335
 Gly Val Gly Leu Ser Pro Asp Arg Met Leu Gln Ala Arg Ile Phe Ala
 340 345 350
 Tyr Ala Asp Gln Gln Arg Tyr Arg Ile Gly Ala Asn Tyr Arg Asp Leu
 355 360 365
 Pro Val Asn Arg Pro Ile Asn Glu Val Asn Thr Tyr Ser Arg Glu Gly
 370 375 380
 Ser Met Gln Tyr Ile Phe Asp Ala Glu Gly Glu Pro Ser Tyr Ser Pro
 385 390 395 400
 Asn Arg Tyr Asp Lys Gly Ala Gly Tyr Leu Asp Asn Gly Thr Asp Ser
 405 410 415
 Ser Ser Asn His Thr Ser Tyr Gly Gln Ala Asp Asp Ile Tyr Val Asn
 420 425 430

Pro Asp Pro His Gly Thr Asp Leu Val Arg Ala Ala Tyr Val Lys His
 435 440 445

Gln Asp Asp Asp Asp Phe Ile Gln Pro Gly Ile Leu Tyr Arg Glu Val
 450 455 460

Leu Asp Glu Gly Glu Lys Glu Arg Leu Ala Asp Asn Ile Ser Asn Ala
 465 470 475 480

Met Gln Gly Ile Ser Glu Ala Thr Glu Pro Arg Val Tyr Asp Tyr Trp
 485 490 495

Asn Asn Val Asp Glu Asn Leu Gly Ala Arg Val Lys Glu Leu Tyr Leu
 500 505 510

Gln Lys Lys Ala
 515

<210> 13

<211> 2439

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2416)

<223> RXA00404

<400> 13

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catttctgca cacagtttct gcccgctgtt tctacgcata gtg gct ttg aaa cga 115
 Val Ala Leu Lys Arg
 1 5

ccc gaa gag aaa aca gta aag atc gtg acc ata aaa cag act gac aac 163
 Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr Asp Asn
 10 15 20

atc aat gac gat gat ttg gtg tac agc aac gct act gac ctt cca gta 211
 Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu Pro Val
 25 30 35

ggc gtg aag aag tcc cct aaa atg tca ccg acc gcc cgc gtt ggt ctc 259
 Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val Gly Leu
 40 45 50

ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc gct ttc 307
 Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile Ala Phe
 55 60 65

tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg gca gtt 355
 Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala Ala Val
 70 75 80 85

ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att gaa tac	403
Gly S r Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr	
90 95 100	
aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa tac gtt	451
Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val	
105 110 115	
aat gac ggc aag gac tat gtc cca acg gat cgt cgt gtg ctt ttt ggc	499
Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu Phe Gly	
120 125 130	
cac cac ttt gca gct att gca ggt gcc ggt cca ttg gtt gga cct gtc	547
His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly Pro Val	
135 140 145	
atg gcc gcg cag atg ggc tac ctg cca ggc acc ttg tgg att atc ctc	595
Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr Leu Trp Ile Ile Leu	
150 155 160 165	
ggt gtg att ttc gcc ggt gca gtg cag gac tac cta gtg ctg tgg gtg	643
Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu Trp Val	
170 175 180	
tct act cgt agg cgt gga cgc tca ctt ggc cag atg gtt cgt gat gaa	691
Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg Asp Glu	
185 190 195	
atg ggc acg gtc ggt gga gct gcc ggt atc ttg gcg acc atc tcc atc	739
Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile	
200 205 210	
atg atc atc att atc gcg gtg ctc gca ttg atc gtg gtt aat gca ctg	787
Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile Val Val Asn Ala Leu	
215 220 225	
gct gat tca cca tgg ggc gtt ttc tcc atc acc atg acc atc cca att	835
Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr Met Thr Ile Pro Ile	
230 235 240 245	
gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt cgt gtt	883
Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val	
250 255 260	
act gaa gtg tcc atc atc ggt gtg gca ctg ctc ctg ctg gct atc gtt	931
Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Leu Ala Ile Val	
265 270 275	
gct ggt ggt tgg gtt gca gac acc tca tgg ggc gtg gaa tgg ttc acc	979
Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp Phe Thr	
280 285 290	
tgg tct aag acc act ttg gcg ttg gcc ttg atc ggt tac gga atc atg	1027
Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met	
295 300 305	
gct gcg att ttg ccg gtg tgg ctg ctg ctt gca ccg cgc gat tac ctg	1075

Ala Ala Il	Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu	
310	315	320 325
tct acc ttt atg aag atc ggc gtc atc ggt ctg ttg gca gtg ggt att		1123
Ser Thr Phe Met	Lys Ile Gly Val Ile Gly Leu Leu Ala Val Gly Ile	
	330 335 340	
ttg ttc gca cgt cct gag gtg cag atg cct tcc gtg acc tcc ttc gca		1171
Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser Val Thr Ser Phe Ala		
	345 350 355	
ctt gag ggc aac ggt ccg gtg ttc tct gga agt ctg ttc cca ttc ctg		1219
Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser Leu Phe Pro Phe Leu		
	360 365 370	
ttc atc acg att gcc tgt ggt gca ctg tct ggt ttc cac gca ctg att		1267
Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly Phe His Ala Leu Ile		
	375 380 385	
tct tca gga acc aca cca aag ctt gtg gag aag gaa tcc cag atg cgc		1315
Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys Glu Ser Gln Met Arg		
	390 395 400 405	
atg ctc ggc tac ggc ggc atg ttg atg gaa tct ttc gtg gcg atg atg		1363
Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser Phe Val Ala Met Met		
	410 415 420	
gca ctg atc acc gct gtt att ctg gat cgt cac ctg tac ttc tcc atg		1411
Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His Leu Tyr Phe Ser Met		
	425 430 435	
aac gct ccg ctg gca ctg act ggt gga gat cca gca acc gca gct gag		1459
Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu		
	440 445 450	
tgg gtt aac tcc att ggg ctg aca ggt gcg gat atc acc ccg gaa cag		1507
Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln		
	455 460 465	
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Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser Thr Val Ile Ser Arg		
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Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met Ser Glu Ile Leu Ser		
	490 495 500	
gga ttc atc ggc ggc gct gga atg aag gcg ttc tgg tac cac ttc gcc		1651
Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe Trp Tyr His Phe Ala		
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Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr Val Asp Ala Gly Thr		
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Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu Gly Asn Val Pro Gly		

535	540	545	
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acc gat cca ctg ggc ggc atc aac gtg ctt ttc cca cta ttc ggt atc Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe Pro Leu Phe Gly Ile 585 590 595			1891
gct aac cag ctg ctc gcc gct att gca ctt gct ctc gtg ctg gtt gtt Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala Leu Val Leu Val Val 600 605 610			1939
gtg gtg aag aag ggc ctg tac aag tgg gcg tgg att cca gct gtt cct Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro 615 620 625			1987
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cgc gat gca aag tct caa ggc ctt acc gaa ttt ggt gcc gct aaa tct Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser 665 670 675			2131
cct gag gca atc gat gcg gtt atc cga aac acc atg att cag ggc atc Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr Met Ile Gln Gly Ile 680 685 690			2179
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act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc atg tgg Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala Met Trp 745 750 755			2371
gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg cac Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser Ser Gly Gly His 760 765 770			2416

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2439

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<211> 772

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<213> Corynebacterium glutamicum

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Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
 35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
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Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
 65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
 85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
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Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
 115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
 130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
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Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
 165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
 180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
 195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile
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Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
 225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
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 Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
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 Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
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 Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
 405 410 415
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 Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
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 Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
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Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
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 Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
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 Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
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 Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
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 Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
 675 680 685
 Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
 690 695 700
 Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
 705 710 715 720
 Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
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 Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
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 Ser Gly Gly His
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<223> RXN03119

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                                         Met  Leu  Asp  Met  Trp
                                         1              5
gag  cac  gct  ttc  tac  ctg  cag  tac  atg  aac  gtt  aag  gca  gat  tac  gtc      163
Glu  His  Ala  Phe  Tyr  Leu  Gln  Tyr  Met  Asn  Val  Lys  Ala  Asp  Tyr  Val
                        10                      15                      20
aag  gct  gtt  tgg  aac  gtc  ttc  aac  tgg  gac  gac  gca  aga  gca  cgc  ttc      211
Lys  Ala  Val  Trp  Asn  Val  Phe  Asn  Trp  Asp  Asp  Ala  Arg  Ala  Arg  Phe
                        25                      30                      35

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 <213> Corynebacterium glutamicum

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 Met Val Glu Arg Asp
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ttc act atc cga cca atc cgc gag ggt gat ttc cct cag gtg agg gac 163
 Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe Pro Gln Val Arg Asp
 10 15 20

atc tac gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct 211
 Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser
 25 30 35

ggg ccc acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc 259
 Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val
 40 45 50

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 Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val
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tct gct gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa 355
 Ser Ala Ala Pro Ile Ser S r Arg Gln Val Phe His Gly Val Val Glu

70	75	80	85	
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Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly	90	95	100	
gct ttg ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg				451
Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp	105	110	115	
tcg atc cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg				499
Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu	120	125	130	
cat gaa tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca				547
His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala	135	140	145	
agg atg ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg				595
Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu	150	155	160	165
tgg gag tgc ctc tta tcc gtt cca gag caa gct caa agt tcc				637
Trp Glu Cys Leu Ser Val Pro Glu Gln Ala Gln Ser Ser	170	175		
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Thr Tyr Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys				
35	40	45		
Ile Met Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe				
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Ile Leu Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe				
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His Gly Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly				
85	90	95		
Arg Gly Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu				
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Ser Asn Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu				

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Gly Ser Ala Lys Leu His	Glu Ser Lys Gly Phe Val	Lys Val Gly Thr
130	135	140
Met His Gln Met Ala Arg	Met Pro Tyr Gly Glu Met	Glu Gly Gln Trp
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Arg Asp Cys Asp Leu Trp	Glu Cys Leu Leu Ser Val	Pro Glu Gln Ala
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Gln Ser Ser		

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 Val Arg Asp Ile Tyr
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 Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val Met Val
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gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg tct gct 259
 Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val Ser Ala
 40 45 50

gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa gat tcc 307
 Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu Asp Ser
 55 60 65

atc tat atc cac ccc cag ggc caa ggc cga gga atc ggc ggc gct ttg 355
 Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly Ala Leu
 70 75 80 85

ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg tcg atc 403
 Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp Ser Ile
 90 95 100

cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg cat gaa 451

His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu His Glu
 105 110 115

tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca agg atg 499
 Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala Arg Met
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ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg tgg gag 547
 Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu Trp Glu
 135 140 145

tgc ctc tta tcc gtt cca gag caa gct caa agt tcc taaagcaatt 593
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 20 25 30

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 35 40 45

Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly
 50 55 60

Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly
 65 70 75 80

Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn
 85 90 95

Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser
 100 105 110

Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His
 115 120 125

Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp
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Ser

<210> 23
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 <212> DNA
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 <223> RXN01345

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                                         Met Arg Phe Gly Leu
                                         1           5

gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac 163
Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Val Asp Arg Gly Asn
                        10                15                20

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Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
                        25                30                35

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg 259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp
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gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc 307
Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe
                        55                60                65

aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac 355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr
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Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala
                        90                95                100

gaa aac gtg gtc act gcg ctg cgt gca ttt cag acg caa ttg gga gat 451
Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp
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acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc 499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser
                        120                125                130

gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc 547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr
                        135                140                145

gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc 595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr
150                155                160                165
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 Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile Lys Ile Pro Phe Asp
 425 430 435

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cca gaa gta gaa gaa acc atc aca gtc aat gac aac ggc gtg gct tcc 1507
 Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp Asn Gly Val Ala Ser
 455 460 465

att tcc atc aag ata ctc ggc ggc gtt acc gtc gag cac aca att 1552
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<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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 35 40 45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
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Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
 65 70 75 80

Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
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Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
 100 105 110

Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
 115 120 125

Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
 130 135 140
 Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
 145 150 155 160
 Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
 165 170 175
 Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
 180 185 190
 Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
 195 200 205
 Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
 210 215 220
 Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
 225 230 235 240
 Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
 245 250 255
 Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
 260 265 270
 Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
 275 280 285
 Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
 290 295 300
 Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
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 Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
 325 330 335
 Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
 340 345 350
 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
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 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
 370 375 380
 Leu Ile Ala Pro Asp Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr
 385 390 395 400
 Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr
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 Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile
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Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile
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Ser Arg Phe Asp Gly Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp
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<211> 1267

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1267)

<223> FRXA01345

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 Met Arg Phe Gly Leu
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 Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Val Asp Arg Gly Asn
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tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc 211
 Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
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att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg 259
 Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp
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gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc 307
 Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe
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aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac 355
 Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr
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ttg ggc gat cat gta cac cct ttg ggc gcc gtc ctg gag gct ttt gcg 403
 Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala
 90 95 100

gaa aac gtg gtc act gcg ctg cgt gca ttt cag acg caa ttg gga gat 451
 Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp
 105 110 115

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Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser	
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Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr	
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gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc	595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr	
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Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp	
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Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala	
215 220 225	
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Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu	
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Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg	
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Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys	
265 270 275	
ttc tac gag gct gcc act ccc ctg gtg gaa aaa tcc ttg tcc atc atg	979
Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys Ser Leu Ser Ile Met	
280 285 290	
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Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly	
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Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu	
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Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser	
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 345 350 355

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 Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu
 360 365 370

cac gat tct ggt cgt gcc gtg agc ttt gac ccg ctg atc gcc ccg gac 1267
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<211> 389

<212> PRT

<213> *Corynebacterium glutamicum*

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 35 40 45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
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Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
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Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
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Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
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Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
 115 120 125

Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
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Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
 145 150 155 160

Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
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Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
 180 185 190

Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
 195 200 205

Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
210 215 220

Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
225 230 235 240

Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
245 250 255

Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
260 265 270

Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
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Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
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Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
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Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
325 330 335

Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
340 345 350

Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
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Leu Ile Ala Pro Asp
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<210> 27

<211> 1308

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1285)

<223> RXA02541

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Val Asn Asn Ser Glu
1 5

tgg gca aat aag aac tat tac gca gac ctg ggg gtc tcc tcg tcc gct 163
Trp Ala Asn Lys Asn Tyr Tyr Ala Asp Leu Gly Val Ser Ser Ser Ala

41

acc gtg cgt atc cca act ggt gtg gaa gat gga cag aaa gtt cgt ctt 883
 Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly Gln Lys Val Arg Leu
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gca ggc caa ggc gaa gca gga cca aat ggc aaa cca gcg ggc gat ctc 931
 Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys Pro Ala Gly Asp Leu
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ttt gtg aaa gtc cac gtg aaa aag gac gat gtg ttc aca cgc gac ggc 979
 Phe Val Lys Val His Val Lys Lys Asp Asp Val Phe Thr Arg Asp Gly
 280 285 290

agc aac att ttg atc acc att ccc gtg agc ttc agc gag ctg gct ttg 1027
 Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe Ser Glu Leu Ala Leu
 295 300 305

ggt ggc gct att tct gtg cca acg ctc aac aag cct gta aaa ctc aag 1075
 Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys Pro Val Lys Leu Lys
 310 315 320 325

cta cct gcg gga acg cca gat ggt cgt act ttg cgt gta cgc ggt cgc 1123
 Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu Arg Val Arg Gly Arg
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 Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu Leu Val Thr Val Gln
 345 350 355

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 Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala Ala Glu Ala Leu Arg
 360 365 370

gca tat gct gaa gca gaa act aat tca ggt ttt gat ccc cgc gct aac 1267
 Ala Tyr Ala Glu Ala Glu Thr Asn Ser Gly Phe Asp Pro Arg Ala Asn
 375 380 385

tgg gcg ggc cag aac cgc tagacgttct ctttgagaaa gga 1308
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<210> 28

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

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Leu Ala Arg Glu Asn His Pro Asp Lys Asn Pro Gly Asp Lys Ala Ala
 35 40 45

Glu Asp Arg Phe Lys Lys Ala Ala Glu Ala Tyr Asp Val Leu Gly Asp
 50 55 60
 Asp Lys Lys Arg Lys Glu Tyr Asp Glu Leu Lys Ala Leu Leu Ala Ser
 65 70 75 80
 Gly Gly Ile Arg Gly Gly Phe Gly Ser Gly Gly Ala Gly Phe Pro Gly
 85 90 95
 Gly Phe Arg Thr Ser Thr Gly Gly Phe Asp Thr Ser Asp Leu Phe Gly
 100 105 110
 Gly Gly Gln Gly Gly Gly Phe Ser Thr Asp Gly Gly Leu Gly Asp Ile
 115 120 125
 Phe Gly Gly Leu Phe Asn Arg Gly Ala Gly Ser His Gln Ser Ala Arg
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 Pro Thr Arg Gly Ala Asp Val Gln Thr Glu Ile Thr Leu Ser Phe Val
 145 150 155 160
 Glu Ala Ala Lys Gly Thr Thr Ile Pro Val Glu Leu Thr Gly Asp Ala
 165 170 175
 Pro Cys Asn Thr Cys His Gly Ser Gly Ser Lys Ser Gly His Pro Ala
 180 185 190
 Lys Cys Gly Thr Cys Asp Gly Thr Gly Phe Thr Ser Glu Asn Lys Gly
 195 200 205
 Ala Phe Gly Phe Ser Ala Pro Cys Ala Thr Cys Gly Gly Thr Gly Glu
 210 215 220
 Ile Ile Thr Asp Pro Cys Asp Asn Cys His Gly Arg Gly Thr Val Arg
 225 230 235 240
 Lys Ser Arg Ser Ile Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly
 245 250 255
 Gln Lys Val Arg Leu Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys
 260 265 270
 Pro Ala Gly Asp Leu Phe Val Lys Val His Val Lys Lys Asp Asp Val
 275 280 285
 Phe Thr Arg Asp Gly Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe
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 Ser Glu Leu Ala Leu Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys
 305 310 315 320
 Pro Val Lys Leu Lys Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu
 325 330 335
 Arg Val Arg Gly Arg Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu
 340 345 350

Leu Val Thr Val Gln Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala
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<210> 29

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(754)

<223> RXA02542

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gga atg ccc gac aat cct ggg gat cct gaa aat acc gat cca gag gca 163
Gly Met Pro Asp Asn Pro Gly Asp Pro Glu Asn Thr Asp Pro Glu Ala
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acc tct gct gat cgt gct gag cag gca gct gaa gaa gca gct gcc cgc 211
Thr Ser Ala Asp Arg Ala Glu Gln Ala Ala Glu Glu Ala Ala Ala Arg
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caa gcg gag gaa tct cca ttt gga cag gcc tca gag gaa gaa att tct 259
Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser Glu Glu Glu Ile Ser
                                     40 45 50
cca gag ctc gaa gca gag atc aat gat ctt cta tca gat gtt gat cca 307
Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu Ser Asp Val Asp Pro
                                     55 60 65
gat ttg gat ggc gat ggt gaa gtg tcc gct gta gaa aca cag ctt gcc 355
Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val Glu Thr Gln Leu Ala
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gaa cgc act gag gat ctg cag cga gtc acc gct gag tac gcc aac tac 403
Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala Glu Tyr Ala Asn Tyr
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cgt cga cgt acc gag cgt gaa cgc cag ggc atc atc gac acc gca cgc 451
Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile Ile Asp Thr Ala Arg
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Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu Asp Asp Leu Asp Leu
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135	140	145	
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Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys Val Glu Ser Phe Gly			
150	155	160	165
gag atc ggc gaa gca ttc gat cca gag atc cac gaa gca gta cag gat			643
Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His Glu Ala Val Gln Asp			
170	175		180
ctc tca cag ggt gat gtc aag gtt ctg gga acg gta ctc cgc aag gga			691
Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr Val Leu Arg Lys Gly			
185	190		195
tac cgc ctc ggc gac cgc gtc atc cgc acc gca atg gtc ctc att ggg			739
Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala Met Val Leu Ile Gly			
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215			

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<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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35 40 45	
Glu Glu Glu Ile Ser Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu	
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Ser Asp Val Asp Pro Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val	
65 70 75 80	
Glu Thr Gln Leu Ala Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala	
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Glu Tyr Ala Asn Tyr Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile	
100 105 110	
Ile Asp Thr Ala Arg Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu	
115 120 125	

Asp Asp Leu Asp Leu Ala Glu Gln His Gly Asp Leu Asn Glu Gly Pro
 130 135 140
 Leu Lys Ser Leu Ser Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys
 145 150 155 160
 Val Glu Ser Phe Gly Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His
 165 170 175
 Glu Ala Val Gln Asp Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr
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<210> 31
 <211> 1977
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1954)
 <223> RXN02543

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 Met Gly Arg Ala Val
 1 5
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20
 ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35
 tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc 259
 Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
 40 45 50
 gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc 307
 Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
 55 60 65
 aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac 355
 Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
 70 75 80 85
 tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc 403

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Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Val	Thr	Asp	Ala	Val	Ile	Thr	
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Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Glu	Ala	
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Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Val	Asn	Glu	Pro	Thr	
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gcg	gct	gca	ctt	gca	tac	ggc	ctt	gag	aag	ggc	gag	cag	gag	cag	acc	595
Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly	Glu	Gln	Glu	Gln	Thr	
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Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser	Leu	Leu	
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Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala	Thr	Ser	Gly	Asp	Asn	
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			215					220					225			
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tcc	tct	tcc	cag	agt	gca	aac	atc	aac	ctt	cct	tac	atc	acc	gtt	gat	883
Ser	Ser	Ser	Gln	Ser	Ala	Asn	Ile	Asn	Leu	Pro	Tyr	Ile	Thr	Val	Asp	
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Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Thr	Leu	Ser	Arg	Ala	Glu	
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Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg	Thr	Lys	Thr	Pro	Phe	
			280					285					290			
aac	cag	gtt	gtt	aag	gac	gct	ggc	gtg	tcc	gtc	tcg	gag	atc	gac	cac	1027
Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val	Ser	Glu	Ile	Asp	His	
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310	315	320	325	
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Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg	345	350	355	
ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc				1219
Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu	360	365	370	
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Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn	375	380	385	
acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac				1315
Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp	390	395	400	405
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Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile	410	415	420	
gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc ggc ggc atc gca				1411
Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala	425	430	435	
cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac				1459
Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp	440	445	450	
gcc aac ggc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag				1507
Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys	455	460	465	
gaa aac acc atc acc att cag gac ggc tcc ggt ctc tcc cag gat gaa				1555
Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu	470	475	480	485
att gat cgc atg atc aag gat gct gaa gct cac gct gat gag gac aag				1603
Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys	490	495	500	
aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt				1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val	505	510	515	
tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa				1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu	520	525	530	
gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca				1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala	535	540	545	

ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg 1795
 Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu
 550 555 560 565

aac acc gag tcc cag gaa atg ggt aag gct atc tac gag gct gac gct 1843
 Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile Tyr Glu Ala Asp Ala
 570 575 580

gct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat 1891
 Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp
 585 590 595

gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat 1939
 Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn
 600 605 610

ggt gag gac aag aag taaatgacta cccctaacgg aat 1977
 Gly Glu Asp Lys Lys
 615

<210> 32

<211> 618

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Met Gly Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
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Ser Val Leu Glu Gly Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly
 20 25 30

Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val
 35 40 45

Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
 50 55 60

Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
 65 70 75 80

Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
 85 90 95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
 100 105 110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
 115 120 125

Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
 130 135 140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
 145 150 155 160

Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
 165 170 175
 Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
 180 185 190
 Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
 195 200 205
 Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
 245 250 255
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
 260 265 270
 Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg
 275 280 285
 Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
 290 295 300
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 305 310 315 320
 Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
 340 345 350
 Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
 385 390 395 400
 Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
 405 410 415
 Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
 420 425 430
 Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
 435 440 445
 Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
 450 455 460

Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly
 465 470 475 480
 Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
 485 490 495
 Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn
 500 505 510
 Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser
 515 520 525
 Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys
 530 535 540
 Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala
 545 550 555 560
 Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile
 565 570 575
 Tyr Glu Ala Asp Ala Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala
 580 585 590
 Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp
 595 600 605
 Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys
 610 615

<210> 33
 <211> 1977
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1954)
 <223> FRXA02543

<400> 33
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 gtggacagta ctaaaatcac ctaaaacagg aggcaccatt atg gga cgt gca gta 115
 Met Gly Arg Ala Val
 1 5
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20
 ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35

tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc	259
Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser	
40 45 50	
gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc	307
Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val	
55 60 65	
aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac	355
Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn	
70 75 80 85	
tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc	403
Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg	
90 95 100	
gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc	451
Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr	
105 110 115	
gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct	499
Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala	
120 125 130	
ggc cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc	547
Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr	
135 140 145	
gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc	595
Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr	
150 155 160 165	
att ctg gta ttc gac ctc ggt ggc ggc acc ttc gac gtc tcc ctc cta	643
Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu	
170 175 180	
gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac	691
Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn	
185 190 195	
gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta	739
Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val	
200 205 210	
gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg	787
Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met	
215 220 225	
gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg	835
Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu	
230 235 240 245	
tcc tct tcc cag agt gca aac atc aac ctt cct tac atc acc gtt gat	883
Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro Tyr Ile Thr Val Asp	
250 255 260	
gca gac aag aac cca ctg ttc ttg gat gag acc ctt tcc cgt gcc gag	931

Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr Leu Ser Arg Ala Glu	
265 270 275	
ttc cag cgc atc acc cag gac ctc ctg gcc cgc acc aag act cct ttc	979
Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg Thr Lys Thr Pro Phe	
280 285 290	
aac cag gtt gtt aag gac gct ggc gtg tcc gtc tcg gag atc gac cac	1027
Asn Gln Val Val Lys Asp Ala Gly Val Ser Val Ser Glu Ile Asp His	
295 300 305	
gtt gtt ctc gtc ggt ggt tcc acc cgt atg cct gct gtt acc gaa ctg	1075
Val Val Leu Val Gly Gly Ser Thr Arg Met Pro Ala Val Thr Glu Leu	
310 315 320 325	
gtc aag gaa ctg acc ggt gga cgt gag cca aac aag ggt gtt aac cca	1123
Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn Lys Gly Val Asn Pro	
330 335 340	
gat gag gtt gtt gca gtt ggt gca gca ctt cag gcc ggt gtt ctc cgc	1171
Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg	
345 350 355	
ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc	1219
Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu	
360 365 370	
ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac	1267
Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn	
375 380 385	
acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac	1315
Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp	
390 395 400 405	
aac cag cct tct gtt cag atc cag gtc ttc cag ggc gag cgt gaa atc	1363
Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile	
410 415 420	
gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc ggc ggc atc gca	1411
Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala	
425 430 435	
cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac	1459
Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp	
440 445 450	
gcc aac ggc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag	1507
Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys	
455 460 465	
gaa aac acc atc acc att cag gac ggc tcc ggt ctc tcc cag gat gaa	1555
Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu	
470 475 480 485	
att gat cgc atg atc aag gat gct gaa gct cac gct gat gag gac aag	1603
Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys	

	490	495	500	
aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt				1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val				
	505	510	515	
tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa				1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu				
	520	525	530	
gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca				1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala				
	535	540	545	
ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg				1795
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu				
	550	555	560	565
aac acc gag tcc cag gaa atg ggt aag gnt atc tnc gag gct gac gct				1843
Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile Xaa Glu Ala Asp Ala				
	570	575	580	
nct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat				1891
Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp				
	585	590	595	
gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat				1939
Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn				
	600	605	610	
ggt gag gac aag aag taaatgacta cccctaacgg aat				1977
Gly Glu Asp Lys Lys				
	615			

<210> 34

<211> 618

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

Met Gly Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val			
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Ser Val Leu Glu Gly Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly			
20 25 30			
Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val			
35 40 45			
Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg			
50 55 60			
Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala			
65 70 75 80			
Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu			

55

385	390	395	400
Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln	405	410	415
Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu	420	425	430
Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val	435	440	445
Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp	450	455	460
Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly	465	470	475
Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His	485	490	495
Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn	500	505	510
Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser	515	520	525
Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys	530	535	540
Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala	545	550	555
Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile	565	570	575
Xaa Glu Ala Asp Ala Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala	580	585	590
Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp	595	600	605
Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys	610	615	

<210> 35

<211> 1947

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1924)

<223> RXN02280

<400> 35

cgcgattgcg tcacgatcg ttgttcttc catgcgcacc acactatctt tctgcacgcc 60

ctgatgccct gtggattcaa aactgtgctt ttataggcgt	atg caa gaa tcc tca	115
	Met Gln Glu Ser Ser	
	1 5	
cggt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt	163	
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser		
10 15 20		
cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag	211	
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln		
25 30 35		
aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc	259	
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly		
40 45 50		
tac gag ccg agt att cgt att ccg ccg gtg acc aag gat cgt gcc acg	307	
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr		
55 60 65		
ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg	355	
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg		
70 75 80 85		
gaa ttg ctg gcg acg gtg ggg ccg acg tcg aaa cgc gat gaa ttc ggt	403	
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly		
90 95 100		
ctg cag ccg gaa ggt ccg ctg ggg caa ttt ggc atc ggg ctg ctt agt	451	
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser		
105 110 115		
tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt	499	
Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly		
120 125 130		
gcg tcg gcg att ccg tgg act ggt cat gcg gat ggc acc ttt aac ctg	547	
Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp Gly Thr Phe Asn Leu		
135 140 145		
gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act	595	
Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr		
150 155 160 165		
gtg cac ctg act ccg ccg cct gat gag ccg acg ttg ctg acg gaa aat	643	
Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn		
170 175 180		
tcc gtg gtc acc att gct agt aat tat ggc ccg tac ctg ccg att cct	691	
Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg Tyr Leu Pro Ile Pro		
185 190 195		
att gtg gtg cag ggt gag aaa aac acc acc atc act aca tcg ccg gtg	739	
Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile Thr Ser Pro Val		
200 205 210		

ttt gca aag gat act gat cag cag cac agg ctg tat gcc ggc cgg gag	787
Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu Tyr Ala Gly Arg Glu	
215 220 225	
cgc ctt ggt aaa act cct ttt gat gtc atc gat ctc acc ggt cct ggc	835
Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp Leu Thr Gly Pro Gly	
230 235 240 245	
atc gag ggt gtg gct tat gta ttg ccg gag gcc cag gct ccg cat atg	883
Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala Gln Ala Pro His Met	
250 255 260	
tcc agg cgt cac agt att tat gtc aac cgc atg ttg gtc tct gat ggg	931
Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met Leu Val Ser Asp Gly	
265 270 275	
cct tcc acg gtg ctg ccc aac tgg gcg ttc ttt gtg gaa tgt gaa atc	979
Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe Val Glu Cys Glu Ile	
280 285 290	
aat tca acc gat ttg gaa ccc acc gca tcg cgt gaa gcg ctc atg gat	1027
Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg Glu Ala Leu Met Asp	
295 300 305	
gac acc gcg ttc gcg gca acc agg gaa cat atc ggt gag tgc att aaa	1075
Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile Gly Glu Cys Ile Lys	
310 315 320 325	
tcg tgg ctg att aat ctc gcc atg acc aag cct cac cgc gtg cgg gaa	1123
Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro His Arg Val Arg Glu	
330 335 340	
ttt act gcg att cat gat ctt gcc ctg cgc gag ctg tgc caa tcg gac	1171
Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu Leu Cys Gln Ser Asp	
345 350 355	
gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc	1219
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser	
360 365 370	
cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag	1267
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu	
375 380 385	
gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc	1315
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu	
390 395 400 405	
aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att	1363
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile	
410 415 420	
cac gac agc gat ctg gct ccg ctc att ccc gtt cac tac cca ccg ctt	1411
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu	
425 430 435	
acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt	1459

Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu	
440 445 450	
ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc	1507
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val	
455 460 465	
acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt	1555
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe	
470 475 480 485	
gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag	1603
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln	
490 495 500	
gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg	1651
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp	
505 510 515	
gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc	1699
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala	
520 525 530	
aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac	1747
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn	
535 540 545	
aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg	1795
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val	
550 555 560 565	
tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag	1843
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys	
570 575 580	
agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca	1891
Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala	
585 590 595	
gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgcta	1944
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile	
600 605	
ctt	1947

<210> 36

<211> 608

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Gln Glu Ser Ser Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val
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Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val
20 25 30

Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
 35 40 45
 Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
 50 55 60
 Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
 65 70 75 80
 Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
 85 90 95
 Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
 100 105 110
 Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
 115 120 125
 Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
 130 135 140
 Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
 145 150 155 160
 Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
 165 170 175
 Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
 180 185 190
 Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
 195 200 205
 Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
 210 215 220
 Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
 225 230 235 240
 Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
 245 250 255
 Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
 260 265 270
 Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe
 275 280 285
 Val Glu Cys Glu Ile Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg
 290 295 300
 Glu Ala Leu Met Asp Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile
 305 310 315 320
 Gly Glu Cys Ile Lys Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro
 325 330 335

His Arg Val Arg Glu Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu
 340 345 350
 Leu Cys Gln Ser Asp Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu
 355 360 365
 Thr Leu Glu Thr Ser Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr
 370 375 380
 Leu Ser Ile Thr Glu Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp
 385 390 395 400
 Asp Phe Arg Gln Leu Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile
 405 410 415
 Asn Gly Gly Tyr Ile His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val
 420 425 430
 His Tyr Pro Pro Leu Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met
 435 440 445
 Asp Leu Met Glu Leu Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala
 450 455 460
 Leu Asp Ala Gln Val Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly
 465 470 475 480
 Ala Thr Arg Val Phe Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile
 485 490 495
 Asp Ser Lys Ala Gln Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala
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 Thr Thr Asp Arg Trp Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu
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 Ser Arg Gln Thr Ala Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu
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 545 550 555 560
 Asp Thr Ala Val Val Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala
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 <222> (101)..(436)
 <223> FRXA02282

<400> 37

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                                         Met Gln Glu Ser Ser
                                         1 5

cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt 163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser
          10          15          20

cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag 211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln
          25          30          35

aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc 259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly
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tac gag ccg agt att cgt att cgg ccg gtg acc aag gat cgt gcc acg 307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr
          55          60          65

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Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg
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gaa ttg ctg gcg acg gtg ggg cgg acg tcg aaa cgc gat gaa ttc ggt 403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly
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ctg cag cgg gaa ggt cgc ctg ggg caa ttt ggc 436
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
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<210> 38
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<400> 38

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				Val	Ala	Arg	Asp	Tyr										
				1				5										
tac	ggc	att	ctc	ggc	gtc	gat	cgc	aat	gca	acc	gaa	tca	gag	atc	aaa	163		
Tyr	Gly	Ile	Leu	Gly	Val	Asp	Arg	Asn	Ala	Thr	Glu	Ser	Glu	Ile	Lys			
			10						15					20				
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Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Arg	Lys	Tyr	His	Pro	Asp	Val	Asn	Pro			
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Gly	Glu	Glu	Ala	Ala	Glu	Lys	Phe	Arg	Glu	Ala	Ser	Val	Ala	His	Glu			
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gta	ctc	act	gat	ccg	gat	aag	cgc	cgc	att	gtt	gat	atg	ggc	ggg	gac	307		
Val	Leu	Thr	Asp	Pro	Asp	Lys	Arg	Arg	Ile	Val	Asp	Met	Gly	Gly	Asp			
	55					60					65							
cca	atg	gag	caa	ggc	ggc	gga	gct	ggc	gct	ggg	ggc	ttc	ggg	gga	ggc	355		
Pro	Met	Glu	Gln	Gly	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Phe	Gly	Gly	Gly			
	70				75					80					85			
ttc	ggc	ggc	agc	ggg	gga	ctg	ggc	gat	atc	ttc	gat	gcc	ttc	ttc	ggc	403		

Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe Asp Ala Phe Phe Gly	
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Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser Arg Val Gln Pro Gly	
105 110 115	
agt gac acc ttg tgg cgc acc tcc atc acc ttg gaa gag gct tac aag	499
Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu Glu Glu Ala Tyr Lys	
120 125 130	
ggc gct aag aaa gat ctc acc ctt gac acc gca gtg ctg tgt acc aag	547
Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala Val Leu Cys Thr Lys	
135 140 145	
tgt cat ggt tct gga tct gca tcc gac aag aag cct gtt acc tgt ggc	595
Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys Pro Val Thr Cys Gly	
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acc tgt aat ggc gct ggt gaa att cag gaa gtg cag cgc agc ttc ctg	643
Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val Gln Arg Ser Phe Leu	
170 175 180	
ggc aac gtc atg acg tcc cgc cca tgc cac acc tgc gat ggc acc ggt	691
Gly Asn Val Met Thr Ser Arg Pro Cys His Thr Cys Asp Gly Thr Gly	
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Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala Ala Asp Gly Arg Val	
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Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro Ala Gly Ile Gln Ser	
215 220 225	
ggc atg cgc atc cgc atg gca ggc caa ggt gag gtt ggc gct ggt ggc	835
Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu Val Gly Ala Gly Gly	
230 235 240 245	
ggt cct gcg ggt gac ctc tac att gaa gtc atg gtg cgc ccg cac gcc	883
Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met Val Arg Pro His Ala	
250 255 260	
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Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala Ser Ile Lys Val Pro	
265 270 275	
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Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp Val Glu Ser Leu Thr	
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ggc gaa gag gtg aaa att acc atc cct gca ggt act cag ccc aac gat	1027
Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly Thr Gln Pro Asn Asp	
295 300 305	
gtg atc acc ttg gat ggt gaa ggc atg ccg aag ctg cgc gca gaa ggc	1075
Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys Leu Arg Ala Glu Gly	

310	315	320	325	
cac ggc aac ctc atg gcg cat gtc gat cta ttt gtg cca acc gat ttg				1123
His Gly Asn Leu Met Ala His Val Asp Leu Phe Val Pro Thr Asp Leu	330	335	340	
gat gac cgc acc cgc gaa ttg ctt gaa gaa atc cgc aac cat cgc agc				1171
Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile Arg Asn His Arg Ser	345	350	355	
gac aac gct tcc gtg cat cgc gaa ggc gga gaa gaa tcc ggt ttc ttt				1219
Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu Glu Ser Gly Phe Phe	360	365	370	
gac aag ctc cga aac aag ttc cgc aaa taatgtcact gccagtattt				1266
Asp Lys Leu Arg Asn Lys Phe Arg Lys	375	380		
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<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Glu	Ser	Glu	Ile	Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Arg	Lys	Tyr	His
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Pro	Asp	Val	Asn	Pro	Gly	Glu	Glu	Ala	Ala	Glu	Lys	Phe	Arg	Glu	Ala
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Ser	Val	Ala	His	Glu	Val	Leu	Thr	Asp	Pro	Asp	Lys	Arg	Arg	Ile	Val
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Asp	Met	Gly	Gly	Asp	Pro	Met	Glu	Gln	Gly	Gly	Gly	Ala	Gly	Ala	Gly
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Gly	Phe	Gly	Gly	Gly	Phe	Gly	Gly	Ser	Gly	Gly	Leu	Gly	Asp	Ile	Phe
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Asp	Ala	Phe	Phe	Gly	Gly	Gly	Ala	Gly	Gly	Ser	Arg	Gly	Pro	Arg	Ser
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Arg	Val	Gln	Pro	Gly	Ser	Asp	Thr	Leu	Trp	Arg	Thr	Ser	Ile	Thr	Leu
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Glu	Glu	Ala	Tyr	Lys	Gly	Ala	Lys	Lys	Asp	Leu	Thr	Leu	Asp	Thr	Ala
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Val	Leu	Cys	Thr	Lys	Cys	His	Gly	Ser	Gly	Ser	Ala	Ser	Asp	Lys	Lys
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Pro Val Thr Cys Gly Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val
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 Gln Arg Ser Phe Leu Gly Asn Val Met Thr Ser Arg Pro Cys His Thr
 180 185 190
 Cys Asp Gly Thr Gly Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala
 195 200 205
 Ala Asp Gly Arg Val Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro
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 Ala Gly Ile Gln Ser Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu
 225 230 235 240
 Val Gly Ala Gly Gly Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met
 245 250 255
 Val Arg Pro His Ala Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala
 260 265 270
 Ser Ile Lys Val Pro Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp
 275 280 285
 Val Glu Ser Leu Thr Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly
 290 295 300
 Thr Gln Pro Asn Asp Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys
 305 310 315 320
 Leu Arg Ala Glu Gly His Gly Asn Leu Met Ala His Val Asp Leu Phe
 325 330 335
 Val Pro Thr Asp Leu Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile
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 Arg Asn His Arg Ser Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu
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 Glu Ser Gly Phe Phe Asp Lys Leu Arg Asn Lys Phe Arg Lys
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<210> 41

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1447)

<223> RXS00568

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Glu	Lys	Leu	Ser	Asp	Thr	Arg	Ser	Lys	Ile	Thr	Val	Glu	Val	Pro	Phe					
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tct	gaa	ctg	aag	cca	gag	atc	gac	cag	gca	tac	gcc	gct	cta	gcg	cag	211				
Ser	Glu	Leu	Lys	Pro	Glu	Ile	Asp	Gln	Ala	Tyr	Ala	Ala	Leu	Ala	Gln					
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caa	gtc	cag	atc	cct	ggt	ttc	cgt	aag	ggc	aag	gca	ccg	cgt	cag	ctt	259				
Gln	Val	Gln	Ile	Pro	Gly	Phe	Arg	Lys	Gly	Lys	Ala	Pro	Arg	Gln	Leu					
				40			45			50										
atc	gac	gca	cgc	ttc	ggc	cgt	ggt	gcg	gtt	ctg	gag	cag	gtt	gtc	aac	307				
Ile	Asp	Ala	Arg	Phe	Gly	Arg	Gly	Ala	Val	Leu	Glu	Gln	Val	Val	Asn					
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gac	atg	ctt	cct	aac	cgc	tac	gca	cag	gca	atc	gaa	gct	gag	ggc	atc	355				
Asp	Met	Leu	Pro	Asn	Arg	Tyr	Ala	Gln	Ala	Ile	Glu	Ala	Glu	Gly	Ile					
				70			75			80			85							
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Lys	Ala	Ile	Gly	Gln	Pro	Asn	Val	Glu	Val	Thr	Lys	Ile	Glu	Asp	Asn					
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Glu	Leu	Val	Glu	Phe	Val	Ala	Glu	Val	Asp	Val	Arg	Pro	Glu	Phe	Glu					
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ctt	cct	aag	ttc	gag	gac	atc	act	gtt	gag	gtc	cca	gct	atc	aag	gct	499				
Leu	Pro	Lys	Phe	Glu	Asp	Ile	Thr	Val	Glu	Val	Pro	Ala	Ile	Lys	Ala					
				120			125			130										
gac	gaa	gag	gca	atc	gaa	gca	gag	ctc	gag	acc	ctg	cgt	gca	cgt	ttc	547				
Asp	Glu	Glu	Ala	Ile	Glu	Ala	Glu	Leu	Glu	Thr	Leu	Arg	Ala	Arg	Phe					
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tcc	acc	ttg	aag	gat	cac	aac	cac	aag	ctg	aag	aag	ggt	gag	ttc	gtc	595				
Ser	Thr	Leu	Lys	Asp	His	Asn	His	Lys	Leu	Lys	Lys	Gly	Glu	Phe	Val					
				150			155			160			165							
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Thr	Ile	Asn	Ile	Thr	Ala	Ser	Ile	Asp	Gly	Glu	Lys	Ile	Glu	Glu	Ala					
				170			175			180										
acc	act	gag	ggt	ctg	tcc	tac	gaa	atc	gga	tct	gac	gat	ctg	att	gac	691				
Thr	Thr	Glu	Gly	Leu	Ser	Tyr	Glu	Ile	Gly	Ser	Asp	Asp	Leu	Ile	Asp					
				185			190			195										
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Gly	Leu	Asp	Lys	Ala	Leu	Ile	Gly	Ala	Lys	Lys	Asp	Glu	Thr	Val	Glu					
				200			205			210										
ttc	acc	tct	gag	ctg	gca	aac	ggc	gag	cac	aag	ggc	aag	gaa	gct	caa	787				
Phe	Thr	Ser	Glu	Leu	Ala	Asn	Gly	Glu	His	Lys	Gly	Lys	Glu	Ala	Gln					

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ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu 265 270 275			931
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aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu 345 350 355			1171
gac acc ctc tct gag gtt gag gag cct gag gtt tcc cag cag gag ctc Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu 360 365 370			1219
acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn 375 380 385			1267
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aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe 425 430 435			1411
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1470

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<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys
 35 40 45

Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu
 50 55 60

Glu Gln Val Val Asn Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile
 65 70 75 80

Glu Ala Glu Gly Ile Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr
 85 90 95

Lys Ile Glu Asp Asn Glu Leu Val Glu Phe Val Ala Glu Val Asp Val
 100 105 110

Arg Pro Glu Phe Glu Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val
 115 120 125

Pro Ala Ile Lys Ala Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr
 130 135 140

Leu Arg Ala Arg Phe Ser Thr Leu Lys Asp His Asn His Lys Leu Lys
 145 150 155 160

Lys Gly Glu Phe Val Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu
 165 170 175

Lys Ile Glu Glu Ala Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser
 180 185 190

Asp Asp Leu Ile Asp Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys
 195 200 205

Asp Glu Thr Val Glu Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys
 210 215 220

Gly Lys Glu Ala Gln Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg
 225 230 235 240

Glu Leu Pro Glu Leu Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe
 245 250 255

Asp Thr Ile Glu Glu Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala
 260 265 270
 Lys Gln Lys Asn Glu Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala
 275 280 285
 Ala Ala Leu Gly Glu Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp
 290 295 300
 Glu Gln Ala His Ser Gln Leu His Gln Leu Leu Gly Glu Leu Ala His
 305 310 315 320
 Asp Asp Ala Ala Leu Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg
 325 330 335
 Glu Glu Phe Asp Lys Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg
 340 345 350
 Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val
 355 360 365
 Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr
 370 375 380
 Gly Met Asp Pro Asn Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln
 385 390 395 400
 Ile Ala Asn Leu Phe Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln
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<210> 43

<211> 826

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(826)

<223> RXN03038

<400> 43

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Met His Ser Lys Glu

1

5

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gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn 40 45 50	259
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ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala 70 75 80 85	355
acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp 90 95 100	403
ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp 105 110 115	451
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cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln 170 175 180	643
aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac Asn Trp Val Thr Arg Thr Asp Leu Glu Leu Thr Ser Asp Asn Asn 185 190 195	691
atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp 200 205 210	739
tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr 215 220 225	787

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 Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala
 230 235 240

826

<210> 44
 <211> 242
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44

Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val
 1 5 10 15

Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr
 20 25 30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
 35 40 45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
 50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
 65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
 85 90 95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
 100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
 115 120 125

Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
 130 135 140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp
 145 150 155 160

Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly
 165 170 175

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu
 180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe
 195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala
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Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val
 225 230 235 240

Ala Ala

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(630)
 <223> RXN03039

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 Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
 20 25 30
 gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg 144
 Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45
 tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca 192
 Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60
 gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc 240
 Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80
 gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat 288
 Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95
 gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga 336
 Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110
 tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt 384
 Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125
 ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg 432
 Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140
 cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg 480
 Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160
 tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac 528
 Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
 165 170 175

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 Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
 180 185 190

tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt 624
 Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
 195 200 205

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 Arg Ala
 210

<210> 46

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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 20 25 30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
 165 170 175

Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
 180 185 190

Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys

195

200

205

Arg Ala
210

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<211> 432
<212> DNA
<213> Corynebacterium glutamicum

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<223> RXN03040

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Met Ser Xaa Gly Asp
1 5

aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg 163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly
10 15 20

ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct 211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala
25 30 35

gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca 259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro
40 45 50

acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc 307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe
55 60 65

ttc ccg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg 355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro
70 75 80 85

atc tat aac cct aac ggt gtg acc tcc agc gag tct tct ntc aga act 403
Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu Ser Ser Xaa Arg Thr
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Val Phe

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<212> PRT
<213> Corynebacterium glutamicum

<400> 48

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 20 25 30
 His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn
 35 40 45
 Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu
 50 55 60
 Ala Leu His Arg Phe Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp
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 Gly Gly Pro Ile Pro Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu
 85 90 95
 Ser Ser Xaa Arg Thr Val Phe
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<210> 49

<211> 835

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(835)

<223> RXN03051

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 Met Arg Ser Asp Val
 1 5
 atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
 Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
 10 15 20
 gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc 211
 Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr
 25 30 35
 ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att. 259
 Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile
 40 45 50
 ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca 307
 Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro
 55 60 65
 ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt 355

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Glu	Phe	Phe	Gly	Gly	Ala	Ile	Tyr	Trp	His	Pro	Asp	Thr	Gly	Ala	Tyr		
			90					95						100			
gca	gtg	acc	ttg	gac	ggt	ttg	cga	cag	tgg	ggg	acc	ttg	aac	tgg	gaa	451	
Ala	Val	Thr	Leu	Asp	Gly	Leu	Arg	Gln	Trp	Gly	Thr	Leu	Asn	Trp	Glu		
			105					110					115				
tca	ggg	cca	ttg	ggg	tac	cca	acc	tct	ggt	ccg	atg	gat	aca	aac	tat	499	
Ser	Gly	Pro	Leu	Gly	Tyr	Pro	Thr	Ser	Gly	Pro	Met	Asp	Thr	Asn	Tyr		
		120					125					130					
ccc	ctt	act	cag	cga	cag	act	ttt	caa	ggt	ggt	gac	aac	tac	tac	aac	547	
Pro	Leu	Thr	Gln	Arg	Gln	Thr	Phe	Gln	Gly	Gly	Asp	Asn	Tyr	Tyr	Asn		
		135				140					145						
cca	ttg	act	ggc	ggt	gct	gtg	tgg	ggc	gat	att	aaa	cag	cgc	tac	gaa	595	
Pro	Leu	Thr	Gly	Gly	Ala	Val	Trp	Gly	Asp	Ile	Lys	Gln	Arg	Tyr	Glu		
150					155				160						165		
gaa	ctt	ggc	ggc	tcg	aat	cat	gcc	att	ggc	atc	ccg	atc	act	aat	gag	643	
Glu	Leu	Gly	Gly	Ser	Asn	His	Ala	Ile	Gly	Ile	Pro	Ile	Thr	Asn	Glu		
				170					175					180			
cta	cct	agc	ggt	act	gag	tat	ttt	tac	aat	aat	ttc	tcc	aat	gga	aca	691	
Leu	Pro	Ser	Gly	Thr	Glu	Tyr	Phe	Tyr	Asn	Asn	Phe	Ser	Asn	Gly	Thr		
			185					190					195				
att	tcg	tgg	cga	aat	gat	cgt	cag	aca	cgg	ttt	atg	tat	ttg	gct	acg	739	
Ile	Ser	Trp	Arg	Asn	Asp	Arg	Gln	Thr	Arg	Phe	Met	Tyr	Leu	Ala	Thr		
		200					205					210					
cag	cgg	gtg	tgg	gat	gcg	ttg	ggt	cgg	gag	acg	ggt	cgt	tta	ggt	ttt	787	
Gln	Arg	Val	Trp	Asp	Ala	Leu	Gly	Arg	Glu	Thr	Gly	Arg	Leu	Gly	Phe		
		215				220					225						
cct	gaa	gca	gat	gaa	aca	cct	gag	gtt	tct	ggt	cta	ttc	cat	gtg	gcg	835	
Pro	Glu	Ala	Asp	Glu	Thr	Pro	Glu	Val	Ser	Gly	Leu	Phe	His	Val	Ala		
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<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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Ala	Asp	Gln	Leu	Glu	Val	Ala	Glu	Ala	Arg	Leu	Asn	Glu	Gly	Ala	Arg		
		20					25						30				

Leu	Met	Ala	Thr	Thr	Gly	Cys	Glu	Val	Met	Trp	Pro	Thr	Gly	Phe	Ser		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

35 40 45
 Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu
 50 55 60
 Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly
 65 70 75 80
 Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro
 85 90 95
 Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly
 100 105 110
 Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro
 115 120 125
 Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly
 130 135 140
 Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile
 145 150 155 160
 Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile
 165 170 175
 Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn
 180 185 190
 Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe
 195 200 205
 Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr
 210 215 220
 Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly
 225 230 235 240
 Leu Phe His Val Ala
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<210> 51

<211> 1704

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1681)

<223> RXN03054

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 Met Lys Leu Phe Ser

1										5									
aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata											163								
Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile																			
gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac											211								
Ala Pro Val Ala Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp																			
caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct											259								
Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro																			
gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc											307								
Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile																			
cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag											355								
His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu																			
ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act											403								
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr																			
att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa											451								
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln																			
caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag											499								
Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Ala Cys Gln																			
acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc											547								
Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg																			
tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa											595								
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu																			
ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg											643								
Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met																			
aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat											691								
Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn																			
aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg											739								
Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp																			
atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg											787								
Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro																			

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ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly 280 285 290	979
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His 295 300 305	1027
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gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro 360 365 370	1219
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aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile 390 395 400 405	1315
caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp 410 415 420	1363
gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp 425 430 435	1411
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 455 460 465

ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt 1555
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
 470 475 480 485

tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag 1603
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
 490 495 500

gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
 505 510 515

gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag 1701
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 520 525

gag 1704

<210> 52
 <211> 527
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 52
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 35 40 45

Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
 50 55 60

Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
 65 70 75 80

Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
 85 90 95

Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
 100 105 110

Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
 115 120 125

Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
 130 135 140

Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met

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Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly	180	185	190
Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly	195	200	205
Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val	210	215	220
Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr	225	230	235
Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln	245	250	255
Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly	260	265	270
Gly Pro Asp Ser Asp Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr	275	280	285
Ala Asp Gly Val Gly Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr	290	295	300
Trp His Pro Gln His Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser	305	310	315
Ile Trp Arg Glu Glu Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile	325	330	335
Gly Asp Pro Glu Lys Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu	340	345	350
Lys Gly Glu Leu Ala Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe	355	360	365
Ile Glu Phe Leu Pro Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe	370	375	380
Glu Asn Gly Leu Ser Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala	385	390	395
Lys Lys Asp Ser Ile Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val	405	410	415
Arg Thr Lys Ser Asp Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe	420	425	430
Lys Ala Arg Met Asp Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val	435	440	445
Gly Tyr Gly Trp Ile Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala			

450

455

460

Ala Tyr Ala Gln Gln Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr
 465 470 475 480

Asn Leu Glu Ala Gly Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly
 485 490 495

Thr Ser Tyr Phe Gln Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln
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Ser Ala Thr Asn Tyr Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
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<210> 53

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> RXN02949

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 Val Ser Asp Glu Gln
 1 5

aat tct ggc gta ggc gga acg tct cgc cca acg ggt aaa cgc cag ctg 163
 Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr Gly Lys Arg Gln Leu
 10 15 20

tcg ggt gct tcc act acc tct acc tct tct tat gag gct aag cag gta 211
 Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr Glu Ala Lys Gln Val
 25 30 35

tct aca cag aag aag tca tcc ggt tcg gat tct aag cct ggc ggc ggt 259
 Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser Lys Pro Gly Gly Gly
 40 45 50

gtt att tct ttt ctg cct gag gtt gtg gga gaa gtc cgt aag gtt att 307
 Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu Val Arg Lys Val Ile
 55 60 65

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 Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr Leu Val Val Leu Gly
 70 75 80 85

ttc ttg att gtt ttg acc gct ttg gtg tct ggt gtg gat ttc cta gct 403
 Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly Val Asp Phe Leu Ala
 90 95 100

ggg ctt gga gtt gag aag att ctg act ccg taggtaggat gtgtaacatc 453

Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
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ttt

456

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 <213> Corynebacterium glutamicum

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 Gly Lys Arg Gln Leu Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr
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 Glu Ala Lys Gln Val Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser
 35 40 45
 Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu
 50 55 60
 Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr
 65 70 75 80
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 100 105 110

<210> 55
 <211> 1941
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1918)
 <223> RXN02462

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 Met Thr Lys Asp Val
 1 5
 cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa 163
 His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
 10 15 20
 ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca 211
 Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala

25	30	35	
cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala 40 45 50			259
cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu 55 60 65			307
gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg 70 75 80 85			355
tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu 90 95 100			403
atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr 105 110 115			451
ttc cgc ctc tac acc aaa ctc gcc ggc atg acc ggt acc gca gag acc Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr 120 125 130			499
gaa gca gca gag ctc aac cag atc tac aag ctc gac gtc atc gcg atc Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile 135 140 145			547
cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr 150 155 160 165			595
aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu 170 175 180			643
cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu 185 190 195			691
cgc tcc gaa tac ctc tcc cag ctg ttg acc aaa cga ggc atc aag cac Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His 200 205 210			739
aac gtc ctc aat gcg aag cac cac gag cag gaa gca cag atc gtt gct Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala 215 220 225			787
cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg ggc Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly 230 235 240 245			835
cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp 250 255 260			883

atc	aaa	ctc	cgc	gaa	cgt	gga	ctt	gat	cct	ttc	gaa	gac	gaa	gaa	agc	931
Ile	Lys	Leu	Arg	Glu	Arg	Gly	Leu	Asp	Pro	Phe	Glu	Asp	Glu	Glu	Ser	
			265					270					275			
tac	cag	gaa	gcc	tgg	gac	gct	gaa	ctt	cca	gca	atg	aag	cag	cga	tgc	979
Tyr	Gln	Glu	Ala	Trp	Asp	Ala	Glu	Leu	Pro	Ala	Met	Lys	Gln	Arg	Cys	
		280					285					290				
gaa	gaa	cgt	ggc	gac	aaa	gtc	cgc	gaa	gcc	gga	gga	ctc	tac	gtc	ctt	1027
Glu	Glu	Arg	Gly	Asp	Lys	Val	Arg	Glu	Ala	Gly	Gly	Leu	Tyr	Val	Leu	
		295				300					305					
ggc	acc	gaa	cgc	cac	gaa	tcc	cga	cgc	atc	gac	aac	cag	ctg	cgc	ggc	1075
Gly	Thr	Glu	Arg	His	Glu	Ser	Arg	Arg	Ile	Asp	Asn	Gln	Leu	Arg	Gly	
310					315					320					325	
cgt	tct	gca	cgt	cag	ggc	gac	cca	gga	tcc	acc	cgc	ttc	tat	ctc	tct	1123
Arg	Ser	Ala	Arg	Gln	Gly	Asp	Pro	Gly	Ser	Thr	Arg	Phe	Tyr	Leu	Ser	
				330				335						340		
atg	cgc	gac	gac	ctg	atg	gtt	cgc	ttc	gtc	ggc	cca	acc	atg	gaa	aac	1171
Met	Arg	Asp	Asp	Leu	Met	Val	Arg	Phe	Val	Gly	Pro	Thr	Met	Glu	Asn	
			345					350					355			
atg	atg	aac	agg	ctc	aac	gtc	cca	gac	gat	gtg	ccc	atc	gaa	tcc	aaa	1219
Met	Met	Asn	Arg	Leu	Asn	Val	Pro	Asp	Asp	Val	Pro	Ile	Glu	Ser	Lys	
		360					365					370				
acc	gtc	acc	aac	tcc	atc	aag	ggc	gcc	caa	gct	cag	gtg	gag	aac	cag	1267
Thr	Val	Thr	Asn	Ser	Ile	Lys	Gly	Ala	Gln	Ala	Gln	Val	Glu	Asn	Gln	
		375				380					385					
aac	ttc	gaa	atg	cgt	aag	aac	gtt	ctg	aag	tac	gac	gaa	gtc	atg	aac	1315
Asn	Phe	Glu	Met	Arg	Lys	Asn	Val	Leu	Lys	Tyr	Asp	Glu	Val	Met	Asn	
390					395					400					405	
gaa	cag	cgc	aag	gtt	atc	tac	agc	gag	cga	cgc	gaa	atc	ctc	gaa	tcc	1363
Glu	Gln	Arg	Lys	Val	Ile	Tyr	Ser	Glu	Arg	Arg	Glu	Ile	Leu	Glu	Ser	
				410				415					420			
gca	gac	atc	tcc	cgc	tac	atc	caa	aac	atg	atc	gaa	gaa	aca	gtc	agc	1411
Ala	Asp	Ile	Ser	Arg	Tyr	Ile	Gln	Asn	Met	Ile	Glu	Glu	Thr	Val	Ser	
			425					430					435			
gca	tac	gtc	gac	ggc	gcc	acc	gcc	aac	ggc	tac	gtc	gaa	gac	tgg	gac	1459
Ala	Tyr	Val	Asp	Gly	Ala	Thr	Ala	Asn	Gly	Tyr	Val	Glu	Asp	Trp	Asp	
		440					445					450				
ctc	gac	aaa	ctc	tgg	aac	gcc	ctc	gaa	gcc	ctc	tac	gac	cca	tcg	atc	1507
Leu	Asp	Lys	Leu	Trp	Asn	Ala	Leu	Glu	Ala	Leu	Tyr	Asp	Pro	Ser	Ile	
	455					460					465					
aac	tgg	acc	gac	ctc	gtc	gaa	ggc	agc	gaa	tac	ggc	aaa	cca	ggg	gag	1555
Asn	Trp	Thr	Asp	Leu	Val	Glu	Gly	Ser	Glu	Tyr	Gly	Lys	Pro	Gly	Glu	
470					475					480					485	

ctg tcc gcc gaa gat cta cgc acc gca ctc gtc aac gac gcc cac gcc 1603
 Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val Asn Asp Ala His Ala
 490 495 500

gaa tac gca aaa ctc gaa gaa gcc gta tcc gca atc ggc ggc gaa gca 1651
 Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala Ile Gly Gly Glu Ala
 505 510 515

cag atc cgc aac atc gaa cga atg gtg ctc atg cca gtc atc gac acc 1699
 Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met Pro Val Ile Asp Thr
 520 525 530

aaa tgg cgc gaa cac ctc tac gaa atg gac tac ctg aaa gaa ggc atc 1747
 Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile
 535 540 545

ggc ctg cgc gca atg gca cag cgc gac cca ctg gtc gaa tac caa aag 1795
 Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys
 550 555 560 565

gaa ggc ggc gac atg ttc aac ggc atg aaa gac ggc atc aag gaa gaa 1843
 Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp Gly Ile Lys Glu Glu
 570 575 580

acc gtc cgc cag ctc ttc ctc tcc gca agc agt tca tca agc aag acg 1891
 Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr
 585 590 595

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atg 1941

<210> 56

<211> 606

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Gly Val Lys Glu Glu Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile
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Asp Asn Leu Tyr Ala Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn
 35 40 45

Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile
 50 55 60

Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
 65 70 75 80

Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala

88

385		390		395		400
Asp Glu Val Met	Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg					
	405			410		415
Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile						
	420			425		430
Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr						
	435			440		445
Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu						
	450			455		460
Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr						
	465			470		475
Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val						
	485			490		495
Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala						
	500			505		510
Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met						
	515			520		525
Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr						
	530			535		540
Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu						
	545			550		555
Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp						
	565			570		575
Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser						
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<211> 1965

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1942)

<223> RXN01559

<400> 57

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 Val Leu Ile Val Val

1															5		
ggt	gtt	tat	gcg	ttg	gtg	ctg	ttg	aca	ggc	gat	cgt	tct	gcc	aca	cca	163	
Gly	Val	Tyr	Ala	Leu	Val	Leu	Leu	Thr	Gly	Asp	Arg	Ser	Ala	Thr	Pro		
				10					15					20			
aaa	ttg	ggt	att	gat	ctg	caa	ggc	gga	acc	cga	gtg	acc	ctc	gtg	ccg	211	
Lys	Leu	Gly	Ile	Asp	Leu	Gln	Gly	Gly	Thr	Arg	Val	Thr	Leu	Val	Pro		
			25					30					35				
cag	ggg	cag	gat	cca	act	cag	gac	cag	ctg	aat	cag	gca	cgc	acc	att	259	
Gln	Gly	Gln	Asp	Pro	Thr	Gln	Asp	Gln	Leu	Asn	Gln	Ala	Arg	Thr	Ile		
			40					45					50				
ctg	gaa	aac	cgt	gtg	aac	ggc	atg	ggc	gtt	tca	ggt	gca	agc	gtg	gtc	307	
Leu	Glu	Asn	Arg	Val	Asn	Gly	Met	Gly	Val	Ser	Gly	Ala	Ser	Val	Val		
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gct	gac	ggt	aac	acg	ctg	gtg	atc	act	gtt	ccc	ggg	gaa	aat	acc	gca	355	
Ala	Asp	Gly	Asn	Thr	Leu	Val	Ile	Thr	Val	Pro	Gly	Glu	Asn	Thr	Ala		
	70					75				80					85		
cag	gcg	caa	tcc	cta	gga	cag	acc	tcc	cag	ctg	ctg	ttc	cgt	ccc	gtt	403	
Gln	Ala	Gln	Ser	Leu	Gly	Gln	Thr	Ser	Gln	Leu	Leu	Phe	Arg	Pro	Val		
				90					95					100			
ggt	cag	gca	gga	atg	ccc	gat	atg	acc	acg	ttg	atg	cca	gag	ctg	gaa	451	
Gly	Gln	Ala	Gly	Met	Pro	Asp	Met	Thr	Thr	Leu	Met	Pro	Glu	Leu	Glu		
			105					110						115			
gag	atg	gcc	aac	agg	tgg	gtt	gaa	tac	ggc	gtc	atc	acc	gaa	gag	cag	499	
Glu	Met	Ala	Asn	Arg	Trp	Val	Glu	Tyr	Gly	Val	Ile	Thr	Glu	Glu	Gln		
		120					125					130					
gca	aat	gcc	tcc	ttg	gag	gaa	atg	aac	acc	gct	gtt	gca	tcg	acc	act	547	
Ala	Asn	Ala	Ser	Leu	Glu	Glu	Met	Asn	Thr	Ala	Val	Ala	Ser	Thr	Thr		
	135						140					145					
gcg	gtg	gaa	ggc	gaa	gaa	gca	act	gag	cca	gaa	ccc	gtc	acc	gtg	tcg	595	
Ala	Val	Glu	Gly	Glu	Glu	Ala	Thr	Glu	Pro	Glu	Pro	Val	Thr	Val	Ser		
	150				155					160					165		
gcg	acc	cct	atg	gat	gag	cca	gcc	aac	tcc	att	gag	gca	aca	cag	cga	643	
Ala	Thr	Pro	Met	Asp	Glu	Pro	Ala	Asn	Ser	Ile	Glu	Ala	Thr	Gln	Arg		
				170					175					180			
cgc	cag	gaa	atc	acg	gac	atg	ctg	cgc	acc	gac	cgc	cag	tcc	acc	gat	691	
Arg	Gln	Glu	Ile	Thr	Asp	Met	Leu	Arg	Thr	Asp	Arg	Gln	Ser	Thr	Asp		
			185					190					195				
ccc	act	gtc	cag	atc	gct	gca	agt	tct	ttg	atg	cag	tgc	acc	act	gat	739	
Pro	Thr	Val	Gln	Ile	Ala	Ala	Ser	Ser	Leu	Met	Gln	Cys	Thr	Thr	Asp		
		200					205					210					
gag	atg	gat	cct	ttg	gcc	ggc	acc	gat	gat	cca	cgc	ctg	cca	ttg	gtg	787	
Glu	Met	Asp	Pro	Leu	Ala	Gly	Thr	Asp	Asp	Pro	Arg	Leu	Pro	Leu	Val		
	215					220					225						

gca tgt gat cca gct gta ggt ggc gtg tat gta ctt gat cct gca cct	835
Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro	
230 235 240 245	
ttg ctc aac ggc gaa acc gat gag gaa aat ggt gcg cgc cta acc ggt	883
Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly	
250 255 260	
aat gag atc gat acc aac cgt ccc atc acc ggt gga ttc aac gcc cag	931
Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln	
265 270 275	
tcc ggc cag atg gaa atc agc ttt gcc ttc aaa tcc ggc gat ggg gaa	979
Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys Ser Gly Asp Gly Glu	
280 285 290	
gaa ggc tct gca act tgg tcc tct ctg acc agc cag tac ctg cag cag	1027
Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln	
295 300 305	
cag atc gcc atc acc ctg gac tct cag gtg att tct gca ccc gtg att	1075
Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile	
310 315 320 325	
cag tca gca acc cct gtg ggt tct gca aca tcc atc acc ggt gac ttc	1123
Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe	
330 335 340	
act caa act gaa gcc caa gat ctg gcg aac aac ctg cgc tac ggt gca	1171
Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala	
345 350 355	
ttg ccc ctg agc ttc gca ggt gaa aac ggc gag cgc ggc gga act acc	1219
Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr	
360 365 370	
acc acc gtt ccg cca tca cta ggc gca gca tcc ttg aag gcc gga ctg	1267
Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu	
375 380 385	
atc gca ggc atc gtc ggc atc gcg ctg gtc gcc atc ttc gtg ttc gcc	1315
Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala	
390 395 400 405	
tac tac cgc gtc ttc gga ttc gtt tcc ctg ttc acc ctg ttt gcc gca	1363
Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala	
410 415 420	
ggc gtg ttg gtc tac ggc ctt ctg gta ctg ctg gga cgc tgg atc gga	1411
Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly	
425 430 435	
tat tcc cta gac ctt gct ggt atc gcc ggt ttg atc atc ggt atc ggt	1459
Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly	
440 445 450	

acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag 1507
 Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu
 455 460 465

 atc cgt gaa gga aga tcc ttt aga tct gca gta cct cgt gca tgg gaa 1555
 Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu
 470 475 480 485

 agc gcc aag cgc acc atc gtc aca ggc aac atg gtc act ttg ctc ggc 1603
 Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly
 490 495 500

 gct atc gtg att tac ttg ctc gcg gtc ggc gaa gtc aag ggc ttt gcc 1651
 Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala
 505 510 515

 ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg 1699
 Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu
 520 525 530

 atc acg gca cca ctg gtt atc ctg gca tca cgc aac cca ttc ttt gcc 1747
 Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala
 535 540 545

 aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa 1795
 Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu
 550 555 560 565

 cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc 1843
 Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile
 570 575 580

 cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc 1891
 His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
 585 590 595

 act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag 1939
 Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu
 600 605 610

 aag tagccatgac tgattcccag act 1965
 Lys

<210> 58

<211> 614

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 58

Val Leu Ile Val Val Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp
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Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg
 20 25 30

Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn
 35 40 45
 Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser
 50 55 60
 Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro
 65 70 75 80
 Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu
 85 90 95
 Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu
 100 105 110
 Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val
 115 120 125
 Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala
 130 135 140
 Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile
 165 170 175
 Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp
 180 185 190
 Arg Gln Ser Thr Asp Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met
 195 200 205
 Gln Cys Thr Thr Asp Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro
 210 215 220
 Arg Leu Pro Leu Val Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val
 225 230 235 240
 Leu Asp Pro Ala Pro Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly
 245 250 255
 Ala Arg Leu Thr Gly Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly
 260 265 270
 Gly Phe Asn Ala Gln Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys
 275 280 285
 Ser Gly Asp Gly Glu Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser
 290 295 300
 Gln Tyr Leu Gln Gln Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile
 305 310 315 320
 Ser Ala Pro Val Ile Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser
 325 330 335

Ile Thr Gly Asp Phe Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn
 340 345 350
 Leu Arg Tyr Gly Ala Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu
 355 360 365
 Arg Gly Gly Thr Thr Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser
 370 375 380
 Leu Lys Ala Gly Leu Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala
 385 390 395 400
 Ile Phe Val Phe Ala Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe
 405 410 415
 Thr Leu Phe Ala Ala Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu
 420 425 430
 Gly Arg Trp Ile Gly Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu
 435 440 445
 Ile Ile Gly Ile Gly Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu
 450 455 460
 Arg Ile Lys Asp Glu Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val
 465 470 475 480
 Pro Arg Ala Trp Glu Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met
 485 490 495
 Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
 500 505 510
 Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
 515 520 525
 Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg
 530 535 540
 Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
 545 550 555 560
 Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
 565 570 575
 Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
 580 585 590
 Thr Asp Asn Ser Ser Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr
 595 600 605
 Asn Gln Glu Glu Glu Lys
 610

<210> 59

<211> 819

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(796)

<223> RXN00046

<400> 59

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acctaaaacg ctgttctcaa cacaggagtt tccttaaata atg gac tta aat act 115
 Met Asp Leu Asn Thr
 1 5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
 Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
 10 15 20

gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
 Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
 25 30 35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
 His Val Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
 40 45 50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307
 Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
 55 60 65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
 Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
 70 75 80 85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
 Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
 90 95 100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
 Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
 105 110 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
 Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
 120 125 130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547
 Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
 135 140 145

ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595
 Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
 150 155 160 165

gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu

	170	175	180	
tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct				691
Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro				
	185	190	195	
gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg				739
Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val				
	200	205	210	
ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca				787
Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser				
	215	220	225	
ctg ttg cac tagcacttag tccagcgctg cac				819
Leu Leu His				
230				

<210> 60

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly				
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Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp				
20	25	30		
Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala				
35	40	45		
Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser				
50	55	60		
Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly				
65	70	75	80	
Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val				
85	90	95		
Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro				
100	105	110		
Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp				
115	120	125		
Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu				
130	135	140		
Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly				
145	150	155	160	
Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu				
165	170	175		

Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
 180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
 195 200 205

Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
 210 215 220

Gly Gln Phe Ala Ser Leu Leu His
 225 230

<210> 61

<211> 1219

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (48)..(1196)

<223> RXN01863

<400> 61

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gtc aaa ttg aag caa cct gtt agc att tac aat gat cca tgg gaa tca 104
 Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser
 5 10 15

tat aac gat gtt aaa gaa cat ggc caa tta act tta agt aac atc gaa 152
 Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu
 20 25 30 35

ttt aca act aca aat ctt tgt aat atg cgt tgt agc cac tgt gca gtt 200
 Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val
 40 45 50

ggt tat act tta caa act gtc gac ccc gag cct tta gat atg gac tta 248
 Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp Met Asp Leu
 55 60 65

att tat cgt aga ctt gat gaa att cca aat ctg cga acg atg tca att 296
 Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr Met Ser Ile
 70 75 80

aca ggt ggc gaa cca atg ttt tct aaa aag tct att aga aat gtt gtt 344
 Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg Asn Val Val
 85 90 95

aaa cct cta tta aag tat gca cat cat cga ggt ata tat aca caa atg 392
 Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr Thr Gln Met
 100 105 110 115

aat tca aac cta aca ttg cct caa gat cgt tat tta gat att gct gaa	440
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu	
120 125 130	
tat atc gat gtt atg cat atc tca cat aac tgg gga aca act gat gaa	488
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Thr Asp Glu	
135 140 145	
ttc gca aat gtt ggc ttt ggc gca atg aag aag caa cca ccg tta aaa	536
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys	
150 155 160	
gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt aca tta	584
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu	
165 170 175	
tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt	632
Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser	
180 185 190 195	
acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg	680
Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met	
200 205 210	
aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca	728
Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala	
215 220 225	
agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat	776
Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His	
230 235 240	
gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act	824
Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr	
245 250 255	
ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta	872
Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu	
260 265 270 275	
tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat	920
Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp	
280 285 290	
ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta	968
Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val	
295 300 305	
act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat	1016
Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp	
310 315 320	
aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa	1064
Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys	
325 330 335	
tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt	1112

Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val
 340 345 350 355
 ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160
 Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu
 360 365 370
 cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 1206
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
 375 380
 taattatgcg gag 1219
 <210> 62
 <211> 383
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 62
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 Trp Glu Ser Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser
 20 25 30
 Asn Ile Glu Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His
 35 40 45
 Cys Ala Val Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp
 50 55 60
 Met Asp Leu Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr
 65 70 75 80
 Met Ser Ile Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg
 85 90 95
 Asn Val Val Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr
 100 105 110
 Thr Gln Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp
 115 120 125
 Ile Ala Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr
 130 135 140
 Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro
 145 150 155 160
 Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala
 165 170 175
 Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu
 180 185 190
 Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val

195					200					205					
His	Asp	Met	Lys	Cys	Ser	Arg	His	Glu	Ile	His	Pro	Met	Tyr	Pro	Ala
210						215				220					
Asp	Phe	Ala	Ser	Gln	Leu	Asn	Val	Leu	Thr	Leu	Ala	Glu	Met	Lys	Lys
225					230					235					240
Thr	Ile	His	Asp	Ile	Leu	Asp	Phe	Arg	Asp	Glu	Asp	Ile	Trp	Met	Leu
			245						250					255	
Phe	Gly	Thr	Leu	Pro	Val	Phe	Pro	Cys	Leu	Lys	Asp	Asp	Glu	Asp	Gln
			260					265					270		
Lys	Leu	Leu	Ser	Arg	Leu	Arg	Asn	Ala	Asn	Asn	Val	Thr	Thr	Arg	Asn
	275						280					285			
Asp	Pro	Asp	Gly	Arg	Ser	Arg	Leu	Asn	Val	Asn	Val	Phe	Thr	Gly	Asn
	290					295					300				
Val	Ile	Val	Thr	Asp	Phe	Gly	Asp	Glu	Thr	Gly	Thr	Ile	Ser	Asn	Ile
305					310					315					320
Gln	Lys	Asp	Lys	Leu	Thr	Asp	Val	Phe	Asp	Lys	Trp	Leu	Ser	Ser	Asp
			325						330					335	
Leu	Ala	Lys	Ser	Leu	Asn	Cys	His	Cys	Ser	Glu	Phe	Ser	Cys	Leu	Gly
			340					345					350		
Pro	Asn	Val	Leu	Val	Lys	Asn	Met	Tyr	Tyr	Pro	Asn	Met	Asp	Phe	Lys
		355					360					365			
Asp	Asn	Glu	Arg	His	Met	His	Lys	Gln	Pro	Gln	Ile	Ile	Gln	Phe	
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<210> 63

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(595)

<223> RXN00833

<400> 63

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                                Met Ala Lys Thr His
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ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
                10                15                20

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gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
 Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
 25 30 35

tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
 Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
 40 45 50

tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
 Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
 55 60 65

gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355
 Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
 70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
 Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
 90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
 Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
 105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499
 Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val
 120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
 Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn
 150 155 160 165

taatttactt cgctcagggg aat 618

<210> 64

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
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Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
 20 25 30

Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60

Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
65 70 75 80

Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
85 90 95

Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
100 105 110

Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
115 120 125

Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
130 135 140

Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
145 150 155 160

Leu Ala Gly Leu Asn
165

<210> 65

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXN01676

<400> 65

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accagcattt tttgcatcct cagtgggtgc tggcccgcgc atg atc ctt cac ggt 115
Met Ile Leu His Gly
1 5

gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt 163
Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
10 15 20

ggg ggc gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc 211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
25 30 35

atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc 259
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
40 45 50

ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt 307
Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
55 60 65

ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta 355
Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu

70	75	80	85	
cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc				403
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu	90	95	100	
ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca				451
Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser	105	110	115	
gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg				499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met	120	125	130	
gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg				547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met	135	140	145	
ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt				595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val	150	155	160	165
tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg				643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp	170	175	180	
tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc				691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr	185	190	195	
cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt				739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe	200	205	210	
gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg				787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp	215	220	225	
aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt				835
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser	230	235	240	245
gga tgg gtt att aac cct cgc taattattag ttttgagcgc agg				879
Gly Trp Val Ile Asn Pro Arg	250			

<210> 66

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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20										25					30															
Gln	Arg	Gln	Thr	Ile	Ile	Val	Val	Ser	Ser	Ile	Val	Leu	Ile	Ile	Leu															
		35					40					45																		
Gly	Phe	Val	Gln	Ile	Phe	Gly	Gly	Gly	Phe	Asp	Phe	Gly	Lys	Ala	Leu															
	50					55					60																			
Pro	Gly	Leu	Asp	Arg	Leu	Gln	Ser	Lys	Ala	Thr	Val	Thr	Ser	Gly	Leu															
65					70					75					80															
Gly	Lys	Ser	Phe	Leu	Leu	Gly	Met	Thr	Ser	Ser	Ile	Ala	Gly	Phe	Cys															
				85				90						95																
Ser	Gly	Pro	Ile	Leu	Gly	Ala	Val	Leu	Thr	Leu	Ala	Ala	Thr	Ser	Gly															
			100					105					110																	
Asn	Ser	Ile	Thr	Ser	Ala	Leu	Ile	Leu	Ser	Ala	Tyr	Gly	Ala	Gly	Met															
		115					120					125																		
Val	Leu	Pro	Leu	Met	Ala	Ile	Ala	Ala	Leu	Trp	Ala	Lys	Leu	Gly	Gln															
	130					135					140																			
Arg	Gly	Gln	Gln	Met	Leu	Arg	Gly	Arg	Glu	Phe	Thr	Phe	Leu	Gly	Arg															
145					150					155					160															
Gln	Trp	His	Ile	Val	Ser	Val	Ile	Ser	Gly	Ala	Leu	Ile	Ile	Ala	Val															
				165					170					175																
Gly	Ile	Leu	Phe	Trp	Ser	Thr	Asn	Gly	Leu	Val	Ser	Met	Pro	Glu	Leu															
			180					185					190																	
Val	Pro	Met	Asp	Thr	Gln	Ile	Trp	Leu	Gln	Glu	Ala	Thr	Phe	Ser	Leu															
		195					200					205																		
Gly	Ser	Pro	Leu	Phe	Asp	Ile	Ala	Leu	Ile	Ile	Val	Ala	Ala	Gly	Leu															
		210				215					220																			
Phe	Leu	Tyr	Phe	Trp	Asn	Lys	Arg	Gln	Lys	Arg	Lys	Glu	Glu	Ala	Gln															
225					230					235					240															
Arg	Pro	Lys	Glu	Ser	Gly	Trp	Val	Ile	Asn	Pro	Arg																			
				245					250																					

<210> 67

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> RXN00380

<400> 67

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	Val Arg Leu Thr Lys	
	1 5	
cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta	163	
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val		
	10 15 20	
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc	211	
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly		
	25 30 35	
gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac	259	
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr		
	40 45 50	
gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc	307	
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu		
	55 60 65	
atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt	355	
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val		
	70 75 80 85	
gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa	403	
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu		
	90 95 100	
tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac	451	
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn		
	105 110 115	
ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac	499	
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr		
	120 125 130	
tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac	547	
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr		
	135 140 145	
cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt	595	
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly		
	150 155 160 165	
gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac	643	
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His		
	170 175 180	
cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg	691	
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu		
	185 190 195	
gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt	741	
Asp Val Ala Leu Pro Leu Val Asp Glu Ala		
	200 205	

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744

<210> 68

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
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Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
 20 25 30

Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
 35 40 45

Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
 50 55 60

Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65 70 75 80

Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
 85 90 95

Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
 100 105 110

Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
 115 120 125

Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
 130 135 140

Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
 145 150 155 160

Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
 165 170 175

Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
 180 185 190

Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
 195 200 205

<210> 69

<211> 495

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(472)

<223> RXN00937

<400> 69

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tctatatata gaccttaciaa atcttgaacg gagattctta atg gca acc atc gat 115
 Met Ala Thr Ile Asp
 1 5

gta acc gaa gaa aca ttt gag agc aca gtt acc ggc gac gga att gtc 163
 Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr Gly Asp Gly Ile Val
 10 15 20

ctc gta gac gca tgg gca tcc tgg tgc gga cct tgc cgc cag ttc gcc 211
 Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro Cys Arg Gln Phe Ala
 25 30 35

cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc 259
 Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala
 40 45 50

aag ctt gat acc gaa gca aac cag ggc ctg gct gca gca ctg cag atc 307
 Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Ala Leu Gln Ile
 55 60 65

cag tcc atc cca act ctg atg gtt ttc cgc gac ggc atc atg gtc tac 355
 Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp Gly Ile Met Val Tyr
 70 75 80 85

cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg gtc aac 403
 Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu Val Asn
 90 95 100

cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc gca gag 451
 Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val Ala Glu
 105 110 115

cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt 495
 Gln Gln Gly Ser Ala Glu Ala
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<210> 70

<211> 124

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 70

Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr
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Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro
 20 25 30

Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr
 35 40 45

Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala
 50 55 60

Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp
 65 70 75 80

Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu
 85 90 95

Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg
 100 105 110

Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala
 115 120

<210> 71
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN02325

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tgcacccgtc taatgaaaat cattactatt aggtgtcatg atg gac cat gca cac 115
 Met Asp His Ala His
 1 5

gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc cag 163
 Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly Gln
 10 15 20

ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg aag 211
 Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly Lys
 25 30 35

gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc atc 259
 Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr Ile
 40 45 50

acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac tcc 307
 Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His Ser
 55 60 65

ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt cag 355
 Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe Gln
 70 75 80 85

gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat cgc 403
 Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp Arg
 90 95 100


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agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg gca 451
Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val Ala
105 110 115

tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc aac 499
Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu Asn
120 125 130

aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa acg 547
Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu Thr
135 140 145

atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg cgc 595
Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro Arg
150 155 160 165

ctg tgg cgg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg gcg 643
Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala Ala
170 175 180

ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag cgg gcg 691
Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg Ala
185 190 195

cac gcg gcg gtg tcg gta ttg gcg cgg atg tct gtg gcg gat cgg gga 739
His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg Gly
200 205 210

gag gat ccg atc gag aag tcg cgc cgg gat cca gac gat gtg aac aag 787
Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn Lys
215 220 225

gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac aca 835
Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr
230 235 240 245

gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc cgg 883
Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg
250 255 260

cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc gca 931
Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala
265 270 275

ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca 977
Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser
280 285

ctttaaatat tct 990

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<210> 72

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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 Glu Val Thr Gly Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala
 20 25 30
 Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn
 35 40 45
 Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val
 50 55 60
 Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp
 65 70 75 80
 Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile
 85 90 95
 Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys
 100 105 110
 Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu
 115 120 125
 Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe
 130 135 140
 Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys
 145 150 155 160
 Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly
 165 170 175
 Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala
 180 185 190
 Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser
 195 200 205
 Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro
 210 215 220
 Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met
 225 230 235 240
 Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys
 245 250 255
 Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro
 260 265 270
 Leu Asp Leu Val Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met
 275 280 285
 Ser

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<210> 73
<211> 900
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(877)  
<223> RXN01837
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				Val	Ser	Thr	Asn	Lys								
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gaa	cga	cgc	caa	cag	gcg	ctt	tcc	cag	ctg	gag	aaa	gaa	atc	aaa	agc	163
Glu	Arg	Arg	Gln	Gln	Ala	Leu	Ser	Gln	Leu	Glu	Lys	Glu	Ile	Lys	Ser	
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cgg	gac	cgc	aaa	gaa	aag	acc	aag	cca	cta	acc	gtg	gtc	ttt	gct	tcc	211
Arg	Asp	Arg	Lys	Glu	Lys	Thr	Lys	Pro	Leu	Thr	Val	Val	Phe	Ala	Ser	
			25					30					35			
ctg	gct	gtc	atc	ctg	gtt	gtc	gtt	ggc	ggt	atc	tgg	tac	gca	gct	acc	259
Leu	Ala	Val	Ile	Leu	Val	Val	Val	Gly	Gly	Ile	Trp	Tyr	Ala	Ala	Thr	
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Arg	Ser	Thr	Glu	Asp	Glu	Val	Ile	Thr	Ala	Asp	Glu	Thr	Ser	Thr	Thr	
	55					60					65					
gca	gag	acc	cct	gac	tac	cag	cca	ctg	gcg	ctg	acc	cgc	acc	acc	gcg	355
Ala	Glu	Thr	Pro	Asp	Tyr	Gln	Pro	Leu	Ala	Leu	Thr	Arg	Thr	Thr	Ala	
70					75					80					85	
ctc	ggc	gac	tcc	gtg	acc	tgt	gag	tac	cca	gat	gct	ggc	gag	gct	tcc	403
Leu	Gly	Asp	Ser	Val	Thr	Cys	Glu	Tyr	Pro	Asp	Ala	Gly	Glu	Ala	Ser	
				90					95					100		
aag	gat	gtc	tcc	aag	cct	gct	act	gaa	aac	gtg	cca	gca	acc	ggc	acc	451
Lys	Asp	Val	Ser	Lys	Pro	Ala	Thr	Glu	Asn	Val	Pro	Ala	Thr	Gly	Thr	
			105					110					115			
gtg	acc	gtc	aac	ctg	acc	acc	gcc	cag	ggc	aac	atc	ggc	atg	gaa	ctt	499
Val	Thr	Val	Asn	Leu	Thr	Thr	Ala	Gln	Gly	Asn	Ile	Gly	Met	Glu	Leu	
		120					125					130				
gat	cgc	tcc	gta	tcc	cct	tgt	acc	gtc	aac	gct	gtt	gag	cac	atg	gct	547
Asp	Arg	Ser	Val	Ser	Pro	Cys	Thr	Val	Asn	Ala	Val	Glu	His	Met	Ala	
	135					140					145					
tcc	gag	ggc	tac	tac	aac	gat	act	gtc	tgc	cac	cgc	atc	acc	acc	tct	595
Ser	Glu	Gly	Tyr	Tyr	Asn	Asp	Thr	Val	Cys	His	Arg	Ile	Thr	Thr	Ser	
150					155					160					165	

ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc 643
 Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly
 170 175 180

ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act 691
 Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr
 185 190 195

gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc 739
 Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala
 200 205 210

aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga 787
 Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val Leu Pro Gln Leu Arg
 215 220 225

gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga 835
 Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu Arg Pro Asp His Arg
 230 235 240 245

aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac 877
 Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg Ser Trp His
 250 255

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<210> 74

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr
 20 25 30

Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile
 35 40 45

Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp
 50 55 60

Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu
 65 70 75 80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
 85 90 95

Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val
 100 105 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn
 115 120 125

Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala
 130 135 140
 Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His
 145 150 155 160
 Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser
 165 170 175
 Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro
 180 185 190
 Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly
 195 200 205
 Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
 210 215 220
 Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
 225 230 235 240
 Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg
 245 250 255
 Ser Trp His

<210> 75
 <211> 741
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(741)
 <223> RXN01926

<400> 75
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 gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc 240

Thr	Leu	Cys	Gln	Leu	Ala	Pro	Ser	Pro	Ala	Gly	Arg	Asp	Ala	Asp	Pro	
65					70					75					80	
aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc	288															
Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr																
	85								90					95		
acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac	336															
Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp																
	100							105					110			
aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa	384															
Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu																
	115						120					125				
ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc	432															
Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe																
	130					135					140					
tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc	480															
Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val																
	145				150				155						160	
gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc	528															
Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala																
	165						170						175			
ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca	576															
Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro																
	180						185						190			
cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa	624															
Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys																
	195					200					205					
tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac	672															
Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp																
	210					215					220					
tcc gaa ggt gtc gtc cag atc ctc aag aac gac ctg cgt ggc gac gcc	720															
Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala																
	225				230				235					240		
aac cca ggt cat ggc cgg tgt	741															
Asn Pro Gly His Gly Arg Cys																
	245															

<210> 76

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
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 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240
 Asn Pro Gly His Gly Arg Cys
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<210> 77

<211> 478

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(478)

<223> RXN02002

<400> 77

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attatggccc agcgcccaca acccgctatt cttaataccc atg agc aac gcc aat 115
Met Ser Asn Ala Asn
1 5
tcc gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta 163
Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Arg Thr Phe Ala Val
10 15 20
atc gca cac ccc gac gcc ggt aaa tcc acc ctc acc gag gca ttg gcg 211
Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala
25 30 35
ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca 259
Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala
40 45 50
ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307
Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg
55 60 65
ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa 355
Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu
70 75 80 85
ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc 403
Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly
90 95 100
cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac 451
His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp
105 110 115
gca gca gtc atg ctt atg cac tcc gtc 478
Ala Ala Val Met Leu Met His Ser Val
120 125

<210> 78

<211> 126

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 78

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Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
20 25 30
Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
35 40 45
Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
50 55 60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
65 70 75 80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu
85 90 95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val
100 105 110

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val
115 120 125

<210> 79

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXN02736

<400> 79

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Met Ile Phe Glu Leu
1 5

ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt 163
Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
10 15 20

gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg 211
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
25 30 35

gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat 259
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
40 45 50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc 307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly
55 60 65

gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc 355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly
70 75 80 85

gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc 403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val
90 95 100

gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc 451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr
105 110 115

ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag 499
 Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln
 120 125 130

gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac 547
 Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr
 135 140 145

gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt 595
 Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly
 150 155 160 165

gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt 643
 Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val
 170 175 180

gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg 691
 Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg
 185 190 195

ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg 739
 Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp
 200 205 210

ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct 787
 Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala
 215 220 225

ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag 835
 Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln
 230 235 240 245

cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat 883
 Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr
 250 255 260

gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca 931
 Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
 265 270 275

tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag 979
 Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
 280 285 290

gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc 1027
 Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
 295 300 305

ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta 1077
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 310 315

tgg 1080

<210> 80

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 80

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Leu Thr Arg Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
 20           25           30

Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
 35           40           45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
 50           55           60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65           70           75           80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
 85           90           95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
 100          105          110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
 115          120          125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
 130          135          140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
 145          150          155          160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
 165          170          175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
 180          185          190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
 195          200          205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
 210          215          220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
 225          230          235          240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
 245          250          255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
 260          265          270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser

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275

280

285

Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
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Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
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<210> 81

<211> 331

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(301)

<223> RXS03217

<400> 81

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tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115
 Met Ala Gln Gly Thr
 1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
 Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
 10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
 Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
 25 30 35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
 Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
 40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
 Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
 55 60 65

taagctctaa ctgctagcta aaaattccgc 331

<210> 82

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
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Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
 20 25 30

Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
 35 40 45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
 50 55 60

Arg Ala Leu
 65

<210> 83

<211> 324

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(301)

<223> FRXA01917

<400> 83

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tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115
 Met Ala Gln Gly Thr
 1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
 Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
 10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
 Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
 25 30 35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
 Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
 40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
 Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
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taagctctaa ctgctagcta aaa 324

<210> 84

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
 20 25 30

Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
 35 40 45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
 50 55 60

Arg Ala Leu
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<210> 85

<211> 504

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(481)

<223> RXA02184

<400> 85

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gaatcagcat atgaattagg aatgaaagtg gtgaggacaa gtg cct gtc gga aca 115
                               Val Pro Val Gly Thr
                               1 5
gtg aag tgg tac gac gcg gag cgt ggt ttc ggc ttt gtc tcc aat cca 163
Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly Phe Val Ser Asn Pro
                10                15                20
ggt ggt gaa gat tgc ttc gta ggt aag caa gta ctt ccc aag gga gtc 211
Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val Leu Pro Lys Gly Val
                25                30                35
acc gaa ttg cac aag gga cag cga atc gat ttt gac ttc gcc gca ggc 259
Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe Asp Phe Ala Ala Gly
                40                45                50
cgt aag ggc cct caa gca ctt cga ata aag att ctt gaa act cca cgc 307
Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile Leu Glu Thr Pro Arg
                55                60                65
agg cgt cca cag cac aaa tac aag cca gaa gag ctc aac gga atg atc 355
Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu Leu Asn Gly Met Ile
                70                75                80                85
tct gac ctc atc acg ctt cta gaa agt gga gtg caa cca ggc ctt gcc 403
Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val Gln Pro Gly Leu Ala
                90                95                100
aaa ggg caa tac ccg gag cac aaa gct gga gcg cag gta gca gaa att 451
Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala Gln Val Ala Glu Ile
                105                110                115
ctt cgc gtt gtt gcg aag gag ctt gag tct taaaacaata aggagaggat 501

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Leu Arg Val Val Ala Lys Glu Leu Glu Ser
120 125

ccg

504

<210> 86

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Val Pro Val Gly Thr Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly
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Phe Val Ser Asn Pro Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val
20 25 30

Leu Pro Lys Gly Val Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe
35 40 45

Asp Phe Ala Ala Gly Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile
50 55 60

Leu Glu Thr Pro Arg Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu
65 70 75 80

Leu Asn Gly Met Ile Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val
85 90 95

Gln Pro Gly Leu Ala Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala
100 105 110

Gln Val Ala Glu Ile Leu Arg Val Val Ala Lys Glu Leu Glu Ser
115 120 125

<210> 87

<211> 324

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(301)

<223> RXA00810

<400> 87

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tcgaaccggt tagtaattcc aatcagtaaa ggtaagacaa atg gca cag ggc act 115
Met Ala Gln Gly Thr
1 5

gtt aag tgg ttc aac cca gag aag ggc ttc ggc ttc atc gct cct tcc 163
Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly Phe Ile Ala Pro Ser
10 15 20

gac gga tcc gct gac gtt ttc gtc cac tac tcc gag atc gag ggc aac 211
Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser Glu Ile Glu Gly Asn
25 30 35

ggc ttc cgt acc ctc gag gag aac cag ctc gtc gag ttc gaa atc ggc 259
Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val Glu Phe Glu Ile Gly
40 45 50

gag ggc gct aag ggc ctt cag gct cag gct gtt cgt gca atc 301
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taattgcatc tgagttcgaa acc 324

<210> 88

<211> 67

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 88

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly
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Phe Ile Ala Pro Ser Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser
20 25 30

Glu Ile Glu Gly Asn Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val
35 40 45

Glu Phe Glu Ile Gly Glu Gly Ala Lys Gly Leu Gln Ala Gln Ala Val
50 55 60

Arg Ala Ile
65

<210> 89

<211> 1017

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (994)

<223> RXA01674

<400> 89

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cggtagacgg tactttcata tccaccata taatgttgat atg gat aat ggg tgg 115
Met Asp Asn Gly Trp
1 5

ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg 163
Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly

10	15	20	
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agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu 40 45 50			259
gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu 55 60 65			307
gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu 70 75 80 85			355
tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly 90 95 100			403
gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp 105 110 115			451
atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn 120 125 130			499
tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly 135 140 145			547
ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val 150 155 160 165			595
caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala 170 175 180			643
aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu 185 190 195			691
ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu 200 205 210			739
ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn 215 220 225			787
gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu 230 235 240 245			835

ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt 883
 Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser
 250 255 260

gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg 931
 Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp
 265 270 275

agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc 979
 Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
 280 285 290

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 Ala Ser Asn His Ile
 295

<210> 90

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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 20 25 30

Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
 35 40 45

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
 50 55 60

Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65 70 75 80

Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
 85 90 95

Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
 100 105 110

Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
 115 120 125

Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
 130 135 140

His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
 145 150 155 160

His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175

Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
 180 185 190
 Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
 195 200 205
 Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
 210 215 220
 Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
 225 230 235 240
 Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu
 245 250 255
 Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro
 260 265 270
 Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly
 275 280 285
 Glu Leu Val Ser Ile Ala Ser Asn His Ile
 290 295

 <210> 91
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(1191)
 <223> RXA02431

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 1 5 10 15
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 Val Phe Gln Ile Val Glu Lys Arg Ala Gly Ile Val Glu Arg Leu Ser
 20 25 30
 atc gat gaa ggc ttc atg gaa cca gag gct ctc gtt gga gcc acc cca 144
 Ile Asp Glu Gly Phe Met Glu Pro Glu Ala Leu Val Gly Ala Thr Pro
 35 40 45
 gaa gag gtg aaa cag tgg gcg gaa gaa tta cgc gcg gaa att aaa gaa 192
 Glu Glu Val Lys Gln Trp Ala Glu Glu Leu Arg Ala Glu Ile Lys Glu
 50 55 60
 gtt act ggc tta ccc tcc tcg gtt ggt gct ggc tcc ggt aag cag atc 240
 Val Thr Gly Leu Pro Ser Ser Val Gly Ala Gly Ser Gly Lys Gln Ile
 65 70 75 80
 gcc aaa att ggt tca ggc gaa gca aag cca gat ggt gtg ttt gtc gtg 288

Ala Lys Ile Gly Ser Gly Glu Ala Lys Pro Asp Gly Val Phe Val Val	
85 90 95	
cca gta gac aag caa cat gac ttg ctt gat cca ctt cct gtg ggc gca	336
Pro Val Asp Lys Gln His Asp Leu Leu Asp Pro Leu Pro Val Gly Ala	
100 105 110	
ctt tgg gga gtg ggt cct gtg aca ggc tcc aag ctt gcc tca atg ggg	384
Leu Trp Gly Val Gly Pro Val Thr Gly Ser Lys Leu Ala Ser Met Gly	
115 120 125	
gtg gaa aca att ggt gat cta gca gcg cta acc caa aaa gaa gta gaa	432
Val Glu Thr Ile Gly Asp Leu Ala Ala Leu Thr Gln Lys Glu Val Glu	
130 135 140	
atc agc ctc ggt gca acc atc gga ata tca ctg tgg aac ctt gcc cga	480
Ile Ser Leu Gly Ala Thr Ile Gly Ile Ser Leu Trp Asn Leu Ala Arg	
145 150 155 160	
gga atc gac gac cgc cct gtg gaa ccc cgc gcc gaa gca aaa cag atc	528
Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile	
165 170 175	
tcc caa gag cac acc tat gaa aaa gac ctc ctc acc agg caa caa gta	576
Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val	
180 185 190	
gat gct gcc atc att cga tca gcc gaa ggc gca cac cga cgg ctc ctc	624
Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu	
195 200 205	
aaa gac gga cgc ggt gcc aga act gtc agc gtg aaa ctg cgg atg gcc	672
Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala	
210 215 220	
gac ttt cgt att gag tct cgt tcc tac acc ttg tcc tat gcc acc gat	720
Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp	
225 230 235 240	
gat tac gca act ctt gag gca aca gca ttc cga ctt gcc cgc tac ccc	768
Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro	
245 250 255	
gga gaa gta ggc ccc atc cgc ctt gtc gga gta agt ttt tct ggt ttg	816
Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu	
260 265 270	
gaa gaa tcc cgc caa gac atc ctc ttc ccg gaa ctt gac caa caa atc	864
Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile	
275 280 285	
atc gta cca cca gca ccc gac acc gat tat gag gta ggc gtg caa tcc	912
Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser	
290 295 300	
tct tct agt tcc gaa agt act caa gtt gaa gcg ccg caa gat gtc gcg	960
Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala	

305	310	315	320	
ttg agt atg tgg tgc gca acg caa gat gtc tac cac cca gaa tat ggc				1008
Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly				
	325	330	335	
cac ggt tgg gta caa ggt gcc ggt cac ggt gtt gta tca gta cgt ttt				1056
His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe				
	340	345	350	
gaa acc cgc agc acc aca aaa ggg cga act aaa agt ttt tcc atg gat				1104
Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp				
	355	360	365	
gac ccg gac ctc acc ccg gca gac cct cta gat agt ttg gat tgg gct				1152
Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala				
	370	375	380	
gac tgg ttt gct gaa aat ggt gaa acg ggg gat gac gaa tagggtttca				1201
Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu				
	385	390	395	
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<400> 92				
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Ile Asp Glu Gly Phe Met Glu Pro Glu Ala Leu Val Gly Ala Thr Pro				
	35	40	45	
Glu Glu Val Lys Gln Trp Ala Glu Glu Leu Arg Ala Glu Ile Lys Glu				
	50	55	60	
Val Thr Gly Leu Pro Ser Ser Val Gly Ala Gly Ser Gly Lys Gln Ile				
	65	70	75	80
Ala Lys Ile Gly Ser Gly Glu Ala Lys Pro Asp Gly Val Phe Val Val				
	85	90	95	
Pro Val Asp Lys Gln His Asp Leu Leu Asp Pro Leu Pro Val Gly Ala				
	100	105	110	
Leu Trp Gly Val Gly Pro Val Thr Gly Ser Lys Leu Ala Ser Met Gly				
	115	120	125	
Val Glu Thr Ile Gly Asp Leu Ala Ala Leu Thr Gln Lys Glu Val Glu				
	130	135	140	

Ile Ser Leu Gly Ala Thr Ile Gly Ile Ser Leu Trp Asn Leu Ala Arg
 145 150 155 160
 Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile
 165 170 175
 Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val
 180 185 190
 Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu
 195 200 205
 Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala
 210 215 220
 Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp
 225 230 235 240
 Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro
 245 250 255
 Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu
 260 265 270
 Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile
 275 280 285
 Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser
 290 295 300
 Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala
 305 310 315 320
 Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly
 325 330 335
 His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe
 340 345 350
 Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp
 355 360 365
 Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala
 370 375 380
 Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu
 385 390 395

<210> 93

<211> 558

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(535)

<223> RXA02446

<400> 93

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gagcgtattc tttgtgttct ctcacgacag gaatactgct atg gcg atc gag tcc 115
 Met Ala Ile Glu Ser
 1 5

atc gcg tac acc agt gaa gca ctc tca acc ggc agt ggc cgg ctg ggg 163
 Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly Ser Gly Arg Leu Gly
 10 15 20

cat gtg cgc tcc aca gat ggt gcg ctc gaa ttt gaa atg aca ccg cca 211
 His Val Arg Ser Thr Asp Gly Ala Leu Phe Glu Met Thr Pro Pro
 25 30 35

aag gct ttg ggc gga tcc ggt gaa ggc acc aat cca gaa cag ctg ttc 259
 Lys Ala Leu Gly Gly Ser Gly Glu Gly Thr Asn Pro Glu Gln Leu Phe
 40 45 50

gcg gta ggt tac gca gcc tgt ttc cac tct gcc atg cac tct gtc gca 307
 Ala Val Gly Tyr Ala Ala Cys Phe His Ser Ala Met His Ser Val Ala
 55 60 65

cgc agc cgc aag atc act ctt gaa gac aca gcg gtt ggt gcc cga gtt 355
 Arg Ser Arg Lys Ile Thr Leu Glu Asp Thr Ala Val Gly Ala Arg Val
 70 75 80 85

agc atc ggg cca aac ggc gct ggt gga ttt gag att gcc gta gaa ctc 403
 Ser Ile Gly Pro Asn Gly Ala Gly Gly Phe Glu Ile Ala Val Glu Leu
 90 95 100

gaa gta tcg att cct caa ttg cca caa gca gaa gcc cag gaa ctt gct 451
 Glu Val Ser Ile Pro Gln Leu Pro Gln Ala Glu Ala Gln Glu Leu Ala
 105 110 115

gat gcc gcg cac cag gtg tgc ccg tat tcc aac gcc aca cga ggc aat 499
 Asp Ala Ala His Gln Val Cys Pro Tyr Ser Asn Ala Thr Arg Gly Asn
 120 125 130

atc tcg gta act gtg tca gtc atc gac gaa gag gct taaaaccaca 545
 Ile Ser Val Thr Val Ser Val Ile Asp Glu Glu Ala
 135 140 145

ggattaacaa aac 558

<210> 94

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 94

Met Ala Ile Glu Ser Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly
 1 5 10 15

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<400> 95
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gaagggtatta atacttcttt aagggtcggg ggattttcgt atg tct act aga aca 115
Met Ser Thr Arg Thr
1 5

acg cca caa gac cgt tat acc gac gaa tac ggc atc gaa cgc gtc aac 163
Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly Ile Glu Arg Val Asn
10 15 20

aag gat gaa ccc ggc ctg gtg gac aaa ctc cgg gac aag cac gac tgg 211
Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg Asp Lys His Asp Trp
25 30 35

ttt gat cat ctc atg cgc atg aat gaa cgt ttc ggc gca aaa ggt ggc 259
Phe Asp His Leu Met Arg Met Asn Glu Arg Phe Gly Ala Lys Gly Gly
40 45 50

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aac caa ttg tcg gcg ggt att acg tat ttc tcc gtg ctg tcg atc ttc Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser Val Leu Ser Ile Phe 55 60 65	307
ccg att gcc atg ctt gtc ttc ggt att gca ggt gtc atc ctt gcc gga Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly Val Ile Leu Ala Gly 70 75 80 85	355
aac cct gaa gtt ctc aca gat att caa aat cga atc aac gat gct tta Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg Ile Asn Asp Ala Leu 90 95 100	403
gaa ggc gag atc ggt aac acc gtc aac ggc atc att gat tcc gcg att Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile Ile Asp Ser Ala Ile 105 110 115	451
gcg cag cgt ggt gct gtg ttg ggc att ggt ggt gta act gcc ctg tgg Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly Val Thr Ala Leu Trp 120 125 130	499
tct gga ctg ggg tgg atg gcg aac ctg cgc ttt gga gtt tcc cgc atg Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met 135 140 145	547
tgg gcc att gac cca act gaa ggc aac ttc att caa aag aag ctc acc Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile Gln Lys Lys Leu Thr 150 155 160 165	595
gac ttg gtc gcg ctg atc gtc ttg ctg ctg gcc atg ggc gta gcc ttc Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala Met Gly Val Ala Phe 170 175 180	643
ggt atc acg gcg ctc ggt gct tcc gga cta acc aaa aac ctg ctg gac Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr Lys Asn Leu Leu Asp 185 190 195	691
ttt gtg ggc ctg ggg gag att ccg ggc att agc tac atc acc tgg gtg Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser Tyr Ile Thr Trp Val 200 205 210	739
gtc gca gca ctt gtt ggt gtc ttg gct aac ttc ctg gtg ttc atg tgg Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe Leu Val Phe Met Trp 215 220 225	787
ctg att ttc tcc ctg cca cgt acc aaa gtt ccc atg aaa ccg ggt ctt Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro Met Lys Pro Gly Leu 230 235 240 245	835
cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val 250 255 260	883
gga tcg ctg ttg gct tca aat gca ttg agt aac ccc gcg ggt gca gca Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn Pro Ala Gly Ala Ala 265 270 275	931

ttc ggt ccg atc atc ggc atc atg gtt gtg ctg tat ttg atc tgg cgc 979
 Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu Tyr Leu Ile Trp Arg
 280 285 290

 atc ctc atg tat tgc tct gcg tgg gct gcc acc agt gaa gaa gcg ttg 1027
 Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr Ser Glu Glu Ala Leu
 295 300 305

 cgt ctt gcg act gtt cca gca cca gag cct gcg atc att cgg gtt cgc 1075
 Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg
 310 315 320 325

 cat gaa att gat cca ggt gaa gaa gtc tcc caa tct gct cga aaa gtg 1123
 His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val
 330 335 340

 ggc att gga gtg gcc gtg ggt gcc gcg act gcg ggt gct ttt gcg ctg 1171
 Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala Gly Ala Phe Ala Leu
 345 350 355

 ttg cgt aaa aaa tagtttttat taagggcatt ccc 1206
 Leu Arg Lys Lys
 360

<210> 96
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 96
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 20 25 30

 Asp Lys His Asp Trp Phe Asp His Leu Met Arg Met Asn Glu Arg Phe
 35 40 45

 Gly Ala Lys Gly Gly Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser
 50 55 60

 Val Leu Ser Ile Phe Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly
 65 70 75 80

 Val Ile Leu Ala Gly Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg
 85 90 95

 Ile Asn Asp Ala Leu Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile
 100 105 110

 Ile Asp Ser Ala Ile Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly
 115 120 125

 Val Thr Ala Leu Trp Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe
 130 135 140

Gly Val Ser Arg Met Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile
 145 150 155 160
 Gln Lys Lys Leu Thr Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala
 165 170 175
 Met Gly Val Ala Phe Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr
 180 185 190
 Lys Asn Leu Leu Asp Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser
 195 200 205
 Tyr Ile Thr Trp Val Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe
 210 215 220
 Leu Val Phe Met Trp Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro
 225 230 235 240
 Met Lys Pro Gly Leu Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu
 245 250 255
 Val Val Lys Gln Val Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn
 260 265 270
 Pro Ala Gly Ala Ala Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu
 275 280 285
 Tyr Leu Ile Trp Arg Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr
 290 295 300
 Ser Glu Glu Ala Leu Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala
 305 310 315 320
 Ile Ile Arg Val Arg His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln
 325 330 335
 Ser Ala Arg Lys Val Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala
 340 345 350
 Gly Ala Phe Ala Leu Leu Arg Lys Lys
 355 360

<210> 97

<211> 753

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(730)

<223> RXA00981

<400> 97

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ggatagaagt acccccagtc cagaatgaag gtcaccacca atg tca gag aat ttg 115
                                   Met Ser Glu Asn Leu
                                   1      5

cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag 163
Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
      10      15      20

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc 211
Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
      25      30      35

att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc 259
Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
      40      45      50

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag 307
Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
      55      60      65

aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc 355
Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
      70      75      80      85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga 403
Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
      90      95      100

atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg 451
Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
      105      110      115

acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct 499
Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
      120      125      130

aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg 547
Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
      135      140      145

cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag 595
Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
      150      155      160      165

atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc 643
Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
      170      175      180

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
      185      190      195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
      200      205      210

gttgaaacca ctg 753

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<210> 98

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

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Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu
      20           25           30

Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
      35           40           45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
      50           55           60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
      65           70           75           80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
      85           90           95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
      100          105          110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
      115          120          125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
      130          135          140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
      145          150          155          160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
      165          170          175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
      180          185          190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
      195          200          205

Val Thr
      210

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<210> 99

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXN00786

<400> 99

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gtctaggtgt ttagcctcaa cgttggatac gctgggaggc atg agc tca cct gtt 115
                                         Met Ser Ser Pro Val
                                         1 5

atc agc ccc gaa acc aaa acc gga aag aag atc ctg ctt gca gcc cct 163
Ile Ser Pro Glu Thr Lys Thr Gly Lys Lys Ile Leu Leu Ala Ala Pro
                        10                        15                        20

cgc gga tac tgt gcc ggc gta gac cgt gca gtg gaa acc gtc gag cgc 211
Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val Glu Thr Val Glu Arg
                        25                        30                        35

gcg ctc gag gaa tac ggc gcc cca att tat gtc cgt aaa gaa atc gtg 259
Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val Arg Lys Glu Ile Val
                        40                        45                        50

cac aac cgt tac gtt gtg gac acc ctg gca gaa aag ggc gcg att ttt 307
His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu Lys Gly Ala Ile Phe
                        55                        60                        65

gtc aac gaa gca tct gaa gca cca gaa ggt gcc aac atg gtg ttc tct 355
Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala Asn Met Val Phe Ser
                        70                        75                        80                        85

gca cac ggc gtg agc cca atg gtc cac gaa gaa gct gca gct aaa aac 403
Ala His Gly Val Ser Pro Met Val His Glu Glu Ala Ala Ala Lys Asn
                        90                        95                        100

atc aag gct att gac gcg gcc tgc ccg ctg gtc acc aaa gtg cac aag 451
Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val Thr Lys Val His Lys
                        105                        110                        115

gaa gtc cag cgc ttt gat aag cag gga ttc cac att ctc ttc atc ggt 499
Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His Ile Leu Phe Ile Gly
                        120                        125                        130

cac gaa ggc cat gaa gaa gta gag ggc acc atg ggt cat tcc gtt gag 547
His Glu Gly His Glu Glu Val Glu Gly Thr Met Gly His Ser Val Glu
                        135                        140                        145

aaa acc cac ctg gtt gac ggc gtt gct ggc att gcc acc ctg cct gaa 595
Lys Thr His Leu Val Asp Gly Val Ala Gly Ile Ala Thr Leu Pro Glu
                        150                        155                        160                        165

ttc tta aac gat gaa cca aac ctg atc tgg ctg tct cag acc acg ctt 643
Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu Ser Gln Thr Thr Leu
                        170                        175                        180

tct gtg gac gag acc atg gag atc gtc cgc gag ctg aag gtg aag ttc 691
Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu Leu Lys Val Lys Phe

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185	190	195	
cct cag ctg cag gat cca ccg tca gat gat att tgc tac gcc acg cag			739
Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile Cys Tyr Ala Thr Gln			
200	205	210	
aac cgc cag gtt gcc gtc aag gct atc gct gag cgc tgc gag ctg atg			787
Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu Arg Cys Glu Leu Met			
215	220	225	
att gtg gtc ggt tcc cgc aac tcc tcc aac tcg gtt cgt ctg gtt gag			835
Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser Val Arg Leu Val Glu			
230	235	240	245
gtc gct aag caa aac ggt gcc gat aac gcc tac ctg gtg gat tac gcc			883
Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr Leu Val Asp Tyr Ala			
250	255	260	
cgc gaa atc gac cca gca tgg ttc gaa ggc gta gag acc atc ggt atc			931
Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val Glu Thr Ile Gly Ile			
265	270	275	
tcc tcc ggc gct tcc gtg cct gag atc ctc gtc cag ggc gtc att gag			979
Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val Gln Gly Val Ile Glu			
280	285	290	
cgc ctg gct gag ttc ggc tac gac gac gtc gag gaa gtc acc tcc gcc			1027
Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu Glu Val Thr Ser Ala			
295	300	305	
gct gag aag att gtt ttc gcg ctg cct cgc gtg ctg cgc cac aag aat			1075
Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val Leu Arg His Lys Asn			
310	315	320	325
taattgcaag aatgaaaaat ccc			1098
<210> 100			
<211> 325			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 100			
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Leu Leu Ala Ala Pro Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val			
20	25	30	
Glu Thr Val Glu Arg Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val			
35	40	45	
Arg Lys Glu Ile Val His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu			
50	55	60	
Lys Gly Ala Ile Phe Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala			
65	70	75	80

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Asn Met Val Phe Ser Ala His Gly Val Ser Pro Met Val His Glu Glu
      85                      90                      95

Ala Ala Ala Lys Asn Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val
      100                      105                      110

Thr Lys Val His Lys Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His
      115                      120                      125

Ile Leu Phe Ile Gly His Glu Gly His Glu Glu Val Glu Gly Thr Met
      130                      135                      140

Gly His Ser Val Glu Lys Thr His Leu Val Asp Gly Val Ala Gly Ile
      145                      150                      155                      160

Ala Thr Leu Pro Glu Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu
      165                      170                      175

Ser Gln Thr Thr Leu Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu
      180                      185                      190

Leu Lys Val Lys Phe Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile
      195                      200                      205

Cys Tyr Ala Thr Gln Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu
      210                      215                      220

Arg Cys Glu Leu Met Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser
      225                      230                      235                      240

Val Arg Leu Val Glu Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr
      245                      250                      255

Leu Val Asp Tyr Ala Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val
      260                      265                      270

Glu Thr Ile Gly Ile Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val
      275                      280                      285

Gln Gly Val Ile Glu Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu
      290                      295                      300

Glu Val Thr Ser Ala Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val
      305                      310                      315                      320

Leu Arg His Lys Asn
      325

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<210> 101

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1108)

<223> RXS01027

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gaactgtgtg	caccacaacg	cggaaggtga	atcgcaccca	atg	gca	aat	aag	aac	115
				Met	Ala	Asn	Lys	Asn	
				1				5	

aat	aag	cct	cat	gag	gtg	gac	aaa	gac	caa	gat	tca	gcc	atg	ctg	atc	163
Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp	Ser	Ala	Met	Leu	Ile	
				10				15						20		

aac	ggt	cgc	ctg	caa	cag	atc	ccg	gcg	cgt	ccc	act	gag	gaa	ttc	acc	211
Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro	Thr	Glu	Glu	Phe	Thr	
			25					30					35			

cgc	cca	act	ctt	gca	gca	ggt	gca	gta	ctg	tgg	cgc	ggc	gac	atc	acc	259
Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp	Arg	Gly	Asp	Ile	Thr	
		40					45					50				

aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cgc	ccg	cac	tat	gat	307
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp	
	55					60					65					

gac	tgg	tcc	ctg	gcc	aag	ggc	aaa	gtc	gat	ccc	ggc	gag	tct	att	ccg	355
Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro	
	70				75					80					85	

aca	acc	gcg	gcc	cgt	gaa	atc	ctt	gaa	gaa	act	ggc	tac	gac	atc	cgt	403
Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg	
			90					95						100		

ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr	
			105					110					115			

aaa	gtg	gtc	tac	tac	tgg	act	gcc	cag	gtt	ctt	ggt	gga	gag	ttt	gtc	499
Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val	
		120					125					130				

ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala	
	135					140					145					

tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala	
	150				155					160				165		

gca	aag	cgt	ttc	cgc	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cgc	643
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg	
			170						175					180		

cat	gct	cat	gca	cat	ggt	cgc	caa	acc	tgg	ggt	ggc	gac	gac	aat	aag	691
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys	
			185				190					195				

cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc 739
 Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro
 200 205 210

 atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat 787
 Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp
 215 220 225

 cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac 835
 Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp
 230 235 240 245

 gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883
 Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
 250 255 260

 gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg 931
 Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
 265 270 275

 ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979
 Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
 280 285 290

 ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa 1027
 Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
 295 300 305

 aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc 1075
 Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
 310 315 320 325

 gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct 1128
 Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 330 335

 cca 1131

<210> 102

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp
 1 5 10 15

 Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro
 20 25 30

 Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
 35 40 45

 Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220
 Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240
 Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255
 Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270
 Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285
 Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
 290 295 300
 Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
 305 310 315 320
 Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 325 330 335

<210> 103

<211> 651
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(628)
 <223> RXS01528

<400> 103

cacccaaacc caaacctctc agtcgaataa gcagaagtct caggacaacc gcaggggtaa 60

gggtcgtagg tctccaacca ggaggcggttc caacacgagg gtg aat cag gcg tgg 115
 Val Asn Gln Ala Trp
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp
 55 60 65

aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
 Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
 70 75 80 85

ggg gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
 Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
 90 95 100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
 Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
 105 110 115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
 Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
 120 125 130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
 Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
 135 140 145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
 Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
 150 155 160 165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648

Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
 170 175

aac

651

<210> 104

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Val Asn Gln Ala Trp Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr
 1 5 10 15

Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
 20 25 30

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
 35 40 45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
 50 55 60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
 65 70 75 80

Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
 85 90 95

Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
 100 105 110

His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu
 115 120 125

Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu
 130 135 140

Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu
 145 150 155 160

Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
 165 170 175

<210> 105

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> RXS01716

<400> 105

gaa gtc act cct gag gga ttc aaa gag atc acc cgt gaa aac acc atc	48
Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile	
1 5 10 15	
ggt cgc ctg ggc aaa ggc gtc gac gcc acc ggt cag cta gac ccc gag	96
Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu	
20 25 30	
gca atc gag cgc act cgt gtc gct ttg gaa aac tac gtt gaa ctc atg	144
Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met	
35 40 45	
gaa acc cat ggg gta gag gcc gta cga atg gtt gcc acc tcc gca acc	192
Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr	
50 55 60	
cgc gat gcg tcc aac cgc gat gaa ttc ttt tcg atg acc cgc cag ctt	240
Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu	
65 70 75 80	
ctg tcc aag atc cgt cct gga tac caa gct gaa gta att tcc ggc gaa	288
Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu	
85 90 95	
gag gaa gct ctg ctg tcc ttc cga ggt gca atc gtt gac ctg cct gaa	336
Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu	
100 105 110	
gac caa ggt cct ttc tgt gtt atc gac ctt ggc ggt gga tcc act gag	384
Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Ser Thr Glu	
115 120 125	
ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc	432
Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr	
130 135 140	
caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca	480
Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro	
145 150 155 160	
ccc gac tgaaaccgaa gtggaaatcg ccc	509
Pro Asp	

<210> 106

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
1 5 10 15

Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
 20 25 30
 Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
 35 40 45
 Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
 50 55 60
 Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
 65 70 75 80
 Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
 85 90 95
 Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
 100 105 110
 Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
 115 120 125
 Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140
 Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160
 Pro Asp

<210> 107
 <211> 654
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(631)
 <223> RXS01835

<400> 107
 tcaacatcta ttctcctgc gatttgc atg ggatatatat taaaaattct agccgaaagt 60
 ttctgcgtg aatacacttt cccgcgcct tcgcaaagct atg aat act gcc gcg 115
 Met Asn Thr Ala Ala
 1 5
 tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
 10 15 20
 agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
 25 30 35
 gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259

Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
 40 45 50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
 55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
 70 75 80 85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
 90 95 100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
 105 110 115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
 120 125 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547
 Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
 150 155 160 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
 170 175

gcggcgctcga taa 654

<210> 108
 <211> 177
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
 Met Asn Thr Ala Ala Trp Ala His Arg His His Val Arg Lys Gly Gly
 1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln

65	70	75	80
Pro Leu Lys S r Trp	Lys Ala Arg Ala Asp	Ala Tyr Leu Leu His Leu	
	85	90	95
Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys			
	100	105	110
Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu			
	115	120	125
Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp			
	130	135	140
Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu			
	145	150	155
Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser			
	165	170	175
Ala			

<210> 109
 <211> 1050
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1027)
 <223> RXS02497

<400> 109
 tcgatgccgc cgctggcgaa gactcgggga aacctaataaa taccgaagaa gaatttgacc 60
 gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
 Val Arg Leu Gly Val
 1 5
 tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
 10 15 20
 ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
 Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
 25 30 35
 ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
 Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
 40 45 50
 aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
 Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
 55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc	355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser	
70 75 80 85	
gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc	403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly	
90 95 100	
gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc	451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe	
105 110 115	
ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac	499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn	
120 125 130	
ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa	547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu	
135 140 145	
tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc	595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr	
150 155 160 165	
cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc	643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu	
170 175 180	
ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg	691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met	
185 190 195	
cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc	739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe	
200 205 210	
cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca	787
Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro	
215 220 225	
cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca	835
His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala	
230 235 240 245	
ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc	883
Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile	
250 255 260	
agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa	931
Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu	
265 270 275	
gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg	979
Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp	
280 285 290	
gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag	1027

Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

taacattttac ccggaagga gtt

1050

<210> 110

<211> 309

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 110

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
 1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
 290 295 300

Asp Lys Gly Leu Glu
 305

<210> 111
 <211> 534
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(511)
 <223> RXS02972

<400> 111
 acctacgacg gtgaaatcct aggtcccccac tcaacccaaa tgggatgcgt gcgcctgacc 60

gaacgaatca tgcgcagcga cccacccgac tgaaaccgaa gtg gaa atc gcc cgc 115
 Val Glu Ile Ala Arg
 1 5

gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att 163
 Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile
 10 15 20

tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc 211
 Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile
 25 30 35

tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac 259
 Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His
 40 45 50

ctc tct gca ctc aac ttc gat gca ctg cga gtt gtc acc gat gag atc 307
 Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile
 55 60 65

att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca 355
 Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro
 70 75 80 85

ggt cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg 403
 Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala
 90 95 100

atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc 451
 Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp Tyr Ile Ile Ile Ser
 105 110 115

gaa aaa gac atc ctc gac ggc ctc atc ctt ggc ctg gta gaa gcc gac 499
 Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly Leu Val Glu Ala Asp
 120 125 130

tct ttg aag aaa taggacccta gttttaaac act 534
 Ser Leu Lys Lys
 135

<210> 112

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Val Glu Ile Ala Arg Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys
 1 5 10 15

Ala Ile Val Pro Ile Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly
 20 25 30

Thr Phe Thr Thr Ile Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp
 35 40 45

Arg Asp Ala Ile His Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val
 50 55 60

Val Thr Asp Glu Ile Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn
 65 70 75 80

Pro Val Val Asp Pro Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val
 85 90 95

Val Val Gln Ala Ala Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp
 100 105 110

Tyr Ile Ile Ile Ser Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly
 115 120 125

Leu Val Glu Ala Asp Ser Leu Lys Lys
 130 135

<210> 113

<211> 636

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXA02159

<400> 113

tgatggacca gcggtccaaag ttttcgatga agcagaaaac cgctccacg ctcagaaagc 60

actgctggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca 115
 Met Ser Leu Gly Ser
 1 5

acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163
 Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg
 10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211
 Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln
 25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259
 Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln
 40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307
 Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg
 55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355
 Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile
 70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403
 Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu
 90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451
 Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu
 105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499
 Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg
 120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547
 Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val
 135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595
 Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu
 150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct 636
 Leu Ser Gly Arg Thr Thr
 170

<210> 114

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

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Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val
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Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln
          20          25          30

Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly
          35          40          45

Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly
          50          55          60

Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly
          65          70          75          80

Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys
          85          90          95

Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly
          100          105          110

Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala
          115          120          125

Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala
          130          135          140

Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys
          145          150          155          160

Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr
          165          170

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<210> 115

<211> 486

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(463)

<223> RXA02201

<400> 115

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agtacttttc gtttgcgctcg gcaatggtgg aaaatctcaa atg gcc gca gcg cta 115
                               Met Ala Ala Ala Leu
                               1          5

gcc aaa aaa cat gcc ggg gac gct ctc aaa gtt tat tca gct ggc aca 163
Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val Tyr Ser Ala Gly Thr
          10          15          20

aag cca ggt acg aaa tta aat caa cag tcc ctt gat tcc att gct gaa 211

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Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu Asp Ser Ile Ala Glu
 25 30 35

gtt ggc gca gat atg tct caa ggg ttt cca aag ggc att gac cag gag 259
 Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys Gly Ile Asp Gln Glu
 40 45 50

tta att aag cga gta gac cgc gtg gtc att ctt ggt gcc gaa gct caa 307
 Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu Gly Ala Glu Ala Gln
 55 60 65

cta gaa atg cct atc gat gca aac ggc ata cta cag cgc tgg gta act 355
 Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu Gln Arg Trp Val Thr
 70 75 80 85

gac gaa ccc tct gaa cgt gga att gaa ggt atg gaa cgc atg cgc ctg 403
 Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met Glu Arg Met Arg Leu
 90 95 100

gtc cga gat gat att gac gcc cga gtc caa aac ctc gtc gct gaa cta 451
 Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn Leu Val Ala Glu Leu
 105 110 115

acc caa aac gca tagcagtttt ctaatctcac aca 486
 Thr Gln Asn Ala
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<210> 116
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 116
 Met Ala Ala Ala Leu Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val
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Tyr Ser Ala Gly Thr Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu
 20 25 30

Asp Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys
 35 40 45

Gly Ile Asp Gln Glu Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu
 50 55 60

Gly Ala Glu Ala Gln Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu
 65 70 75 80

Gln Arg Trp Val Thr Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met
 85 90 95

Glu Arg Met Arg Leu Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn
 100 105 110

Leu Val Ala Glu Leu Thr Gln Asn Ala
 115 120

<213> Corynebacterium glutamicum

<400> 118

Met Lys Ser Val Leu Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln
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Met Ala Ala Ala Leu Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile
 20 25 30

His Ser Ala Gly Thr Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val
 35 40 45

Glu Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys
 50 55 60

Ala Ile Asp Pro Glu Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu
 65 70 75 80

Gly Asp Asp Ala Gln Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu
 85 90 95

Glu Arg Trp Ser Ile Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met
 100 105 110

Arg Ile Val Arg Asp Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala
 115 120 125

Gly

<210> 119

<211> 1221

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1198)

<223> RXA00600

<400> 119

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catcgatatt gaaggtatatt ttatatcggc aaacatcaat atg att gaa ggc tgg 115
 Met Ile Glu Gly Trp
 1 5

ctc atg acc ctt act aaa gag cat tcg aca cct cga gcg gct ggc tca 163
 Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro Arg Ala Ala Gly Ser
 10 15 20

atg tcg ttt ctt gac cgc tgg tta gct gcc tgg att ttc ttg gct atg 211
 Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp Ile Phe Leu Ala Met
 25 30 35

gct gct ggg ttg tta atc ggc aag gtc ttt cca gga att ggg gcg ctt 259

Ala	Ala	Gly	Leu	Leu	Ile	Gly	Lys	Val	Phe	Pro	Gly	Ile	Gly	Ala	Leu		
	40						45					50					
ttg	agc	gcg	gtg	gaa	att	ggt	gga	att	tcc	att	cca	att	gct	atc	ggt	307	
Leu	Ser	Ala	Val	Glu	Ile	Gly	Gly	Ile	Ser	Ile	Pro	Ile	Ala	Ile	Gly		
	55					60					65						
ttg	atc	gtc	atg	atg	tat	cca	cct	ttg	gcc	aag	gtg	cgc	tac	gac	aaa	355	
Leu	Ile	Val	Met	Met	Tyr	Pro	Pro	Leu	Ala	Lys	Val	Arg	Tyr	Asp	Lys		
	70				75				80						85		
act	aaa	gaa	atc	agc	aca	gac	cgc	gct	ctc	atg	gtg	gtg	tcg	att	atg	403	
Thr	Lys	Glu	Ile	Ser	Thr	Asp	Arg	Ala	Leu	Met	Val	Val	Ser	Ile	Met		
				90				95						100			
ttg	aac	tgg	atc	gtt	gga	cca	gca	ctt	atg	ttt	agc	ctg	gcg	tgg	ctg	451	
Leu	Asn	Trp	Ile	Val	Gly	Pro	Ala	Leu	Met	Phe	Ser	Leu	Ala	Trp	Leu		
			105					110					115				
ttt	ctt	cca	gat	caa	cca	gag	ctt	cgc	act	ggg	cta	att	atc	gtg	ggc	499	
Phe	Leu	Pro	Asp	Gln	Pro	Glu	Leu	Arg	Thr	Gly	Leu	Ile	Ile	Val	Gly		
		120					125					130					
ctt	gcg	cgc	tgt	atc	gcg	atg	gtt	ttg	gta	tgg	agt	gat	ctc	gct	tgt	547	
Leu	Ala	Arg	Cys	Ile	Ala	Met	Val	Leu	Val	Trp	Ser	Asp	Leu	Ala	Cys		
	135					140					145						
ggt	gac	cgg	gaa	gca	act	gct	gtg	ctg	gtt	gca	atc	aac	tcg	gtg	ttc	595	
Gly	Asp	Arg	Glu	Ala	Thr	Ala	Val	Leu	Val	Ala	Ile	Asn	Ser	Val	Phe		
	150				155					160					165		
cag	atc	ctt	atg	ttc	ggt	gtg	ctt	ggt	tgg	ttt	tac	ctg	cag	att	ctt	643	
Gln	Ile	Leu	Met	Phe	Gly	Val	Leu	Gly	Trp	Phe	Tyr	Leu	Gln	Ile	Leu		
				170					175					180			
ccc	tcg	tgg	ctg	gga	tta	gac	acc	acg	tcg	gtg	act	ttc	tct	gtg	gta	691	
Pro	Ser	Trp	Leu	Gly	Leu	Asp	Thr	Thr	Ser	Val	Thr	Phe	Ser	Val	Val		
			185					190					195				
tca	atc	gtg	act	tcc	gtt	ctc	gtg	ttc	ttg	ggc	ata	cca	ctt	gta	gct	739	
Ser	Ile	Val	Thr	Ser	Val	Leu	Val	Phe	Leu	Gly	Ile	Pro	Leu	Val	Ala		
		200					205					210					
gga	gtt	tta	tct	cgc	gtc	att	ggt	gaa	aaa	aca	aag	gga	cgg	cgc	tgg	787	
Gly	Val	Leu	Ser	Arg	Val	Ile	Gly	Glu	Lys	Thr	Lys	Gly	Arg	Arg	Trp		
	215					220					225						
tac	gag	gac	acg	ttc	ctg	cct	aag	att	tca	ccc	ttg	gcg	ctg	att	ggc	835	
Tyr	Glu	Asp	Thr	Phe	Leu	Pro	Lys	Ile	Ser	Pro	Leu	Ala	Leu	Ile	Gly		
	230				235					240					245		
ttg	cta	tac	aca	att	gtt	ctg	ctg	ttt	tcg	ttg	cag	ggg	gat	gaa	atc	883	
Leu	Leu	Tyr	Thr	Ile	Val	Leu	Leu	Phe	Ser	Leu	Gln	Gly	Asp	Glu	Ile		
				250					255					260			
aca	gcg	cag	cct	tgg	aca	gta	gct	cgt	ctt	gca	ttg	ccg	ctg	ctg	atg	931	
Thr	Ala	Gln	Pro	Trp	Thr	Val	Ala	Arg	Leu	Ala	Leu	Pro	Leu	Leu	Met		

265	270	275	
tac ttt gtg ggc atg ttt ttc att tcc ctg gtg gta tcc aaa ctg tcc			979
Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val Val Ser Lys Leu Ser			
280	285	290	
ggg tta act tat gag cga gct gct tcc gtg tct ttt act gca gca gga			1027
Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser Phe Thr Ala Ala Gly			
295	300	305	
aac aac ttt gaa tta gcg att gcg gta tcg atc gga acc ttt ggt gcg			1075
Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala			
310	315	320	325
aca tca ccg cag gca tta gct gga acg atc ggc cct ttg att gaa gtc			1123
Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly Pro Leu Ile Glu Val			
330	335		340
cca gta tta gtc gga ttg gtt tat gtc atg ttg tgg ctt gga cca aaa			1171
Pro Val Leu Val Gly Leu Val Tyr Val Met Leu Trp Leu Gly Pro Lys			
345	350		355
atc ttt aaa aag gag aat gca gga tca tgaaatcagt tttgtttgtg			1218
Ile Phe Lys Lys Glu Asn Ala Gly Ser			
360	365		
tgc			1221

<210> 120

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Met	Ile	Glu	Gly	Trp	Leu	Met	Thr	Leu	Thr	Lys	Glu	His	Ser	Thr	Pro
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Arg	Ala	Ala	Gly	Ser	Met	Ser	Phe	Leu	Asp	Arg	Trp	Leu	Ala	Ala	Trp
			20						25				30		

Ile	Phe	Leu	Ala	Met	Ala	Ala	Gly	Leu	Leu	Ile	Gly	Lys	Val	Phe	Pro
			35				40					45			

Gly	Ile	Gly	Ala	Leu	Leu	Ser	Ala	Val	Glu	Ile	Gly	Gly	Ile	Ser	Ile
	50					55					60				

Pro	Ile	Ala	Ile	Gly	Leu	Ile	Val	Met	Met	Tyr	Pro	Pro	Leu	Ala	Lys
65					70					75					80

Val	Arg	Tyr	Asp	Lys	Thr	Lys	Glu	Ile	Ser	Thr	Asp	Arg	Ala	Leu	Met
				85					90					95	

Val	Val	Ser	Ile	Met	Leu	Asn	Trp	Ile	Val	Gly	Pro	Ala	Leu	Met	Phe
			100					105					110		

Ser	Leu	Ala	Trp	Leu	Phe	Leu	Pro	Asp	Gln	Pro	Glu	Leu	Arg	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val Leu Val Trp 130 135 140		
Ser Asp Leu Ala Cys Gly Asp Arg Glu Ala Thr Ala Val Leu Val Ala 145 150 155 160		
Ile Asn Ser Val Phe Gln Ile Leu Met Phe Gly Val Leu Gly Trp Phe 165 170 175		
Tyr Leu Gln Ile Leu Pro Ser Trp Leu Gly Leu Asp Thr Thr Ser Val 180 185 190		
Thr Phe Ser Val Val Ser Ile Val Thr Ser Val Leu Val Phe Leu Gly 195 200 205		
Ile Pro Leu Val Ala Gly Val Leu Ser Arg Val Ile Gly Glu Lys Thr 210 215 220		
Lys Gly Arg Arg Trp Tyr Glu Asp Thr Phe Leu Pro Lys Ile Ser Pro 225 230 235 240		
Leu Ala Leu Ile Gly Leu Leu Tyr Thr Ile Val Leu Leu Phe Ser Leu 245 250 255		
Gln Gly Asp Glu Ile Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala 260 265 270		
Leu Pro Leu Leu Met Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val 275 280 285		
Val Ser Lys Leu Ser Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser 290 295 300		
Phe Thr Ala Ala Gly Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile 305 310 315 320		
Gly Thr Phe Gly Ala Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly 325 330 335		
Pro Leu Ile Glu Val Pro Val Leu Val Gly Leu Val Tyr Val Met Leu 340 345 350		
Trp Leu Gly Pro Lys Ile Phe Lys Lys Glu Asn Ala Gly Ser 355 360 365		

<210> 121

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> RXA02200

<400> 121
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tttgaatatc gacaggtatc aatataccga aaggtgtcgc atg aca aac tca act 115
Met Thr Asn Ser Thr
1 5

cag acg cgg gcc aag cca gcc cga atc tca ttt ctt gat aaa tac att 163
Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe Leu Asp Lys Tyr Ile
10 15 20

cca ctt tgg att att ttg gcg atg gcg ttt ggg cta ttt tta ggc cgg 211
Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly Leu Phe Leu Gly Arg
25 30 35

agc gtt tcg gga ctc tca ggc ttt cta ggc gca atg gaa gtc gga ggg 259
Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala Met Glu Val Gly Gly
40 45 50

atc tcc ttg cca atc gct tta ggc ctc ctt gta atg atg tac cca ccg 307
Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val Met Met Tyr Pro Pro
55 60 65

ttg gcc aaa gtt cgg tat gac aaa act aaa caa att gcc act gat aag 355
Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln Ile Ala Thr Asp Lys
70 75 80 85

cat ttg atg ggc gtg tca ctc att ctc aat tgg gtg gtg ggt cct gcc 403
His Leu Met Gly Val Ser Leu Ile Leu Asn Trp Val Val Gly Pro Ala
90 95 100

tta atg ttc gcg cta gct tgg ttg ttc ctc cca gac caa ccg gaa tta 451
Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu
105 110 115

cga acc ggc ctg att att gta gga ctc gca cga tgt att gcg atg gtc 499
Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val
120 125 130

ttg gtt tgg tct gat atg tcc tgt gga gac cgc gag gct aca gca gtt 547
Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg Glu Ala Thr Ala Val
135 140 145

ctc gta gcc att aat tca gtt ttt caa gtc gca atg ttt ggt gca ctt 595
Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala Met Phe Gly Ala Leu
150 155 160 165

ggc tgg ttc tat ctg caa gtt tta cca tcc tgg cta gga tta cca act 643
Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp Leu Gly Leu Pro Thr
170 175 180

acc acc gct caa ttc tct ttc tgg tca att gtg act tcg gtt ttg gtg 691
Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val Thr Ser Val Leu Val
185 190 195

ttc ctc gga ata cct cta ctt gct gga gtt ttc tcg cga att att ggc 739

Phe	Leu	Gly	Ile	Pro	Leu	Leu	Ala	Gly	Val	Phe	Ser	Arg	Ile	Ile	Gly		
	200						205					210					
gaa	aag	atc	aag	gga	cgt	gag	tgg	tat	gaa	caa	aag	ttc	ctt	ccg	gca	787	
Glu	Lys	Ile	Lys	Gly	Arg	Glu	Trp	Tyr	Glu	Gln	Lys	Phe	Leu	Pro	Ala		
	215					220					225						
atc	tct	cca	ttt	gca	cta	atc	ggg	ctg	ctt	tat	acg	atc	gtc	ttg	ttg	835	
Ile	Ser	Pro	Phe	Ala	Leu	Ile	Gly	Leu	Leu	Tyr	Thr	Ile	Val	Leu	Leu		
	230				235					240					245		
ttt	tca	ttg	caa	ggg	gat	cag	atc	gtc	tct	caa	cca	tgg	gct	gta	gtt	883	
Phe	Ser	Leu	Gln	Gly	Asp	Gln	Ile	Val	Ser	Gln	Pro	Trp	Ala	Val	Val		
				250					255					260			
cgt	ctc	gcg	ata	cca	ttg	gtt	atc	tat	ttc	gtt	gga	atg	ttt	ttc	att	931	
Arg	Leu	Ala	Ile	Pro	Leu	Val	Ile	Tyr	Phe	Val	Gly	Met	Phe	Phe	Ile		
			265					270					275				
tca	ctc	att	gcg	tca	aaa	cta	tct	ggc	atg	aac	tat	gca	aag	tct	gca	979	
Ser	Leu	Ile	Ala	Ser	Lys	Leu	Ser	Gly	Met	Asn	Tyr	Ala	Lys	Ser	Ala		
		280					285					290					
tcc	gtc	tct	ttc	act	gca	gct	ggc	aac	aat	ttt	gaa	ctt	gcg	att	gcg	1027	
S r	Val	Ser	Phe	Thr	Ala	Ala	Gly	Asn	Asn	Phe	Glu	Leu	Ala	Ile	Ala		
	295					300					305						
gtg	tcg	atc	gga	acg	ttt	ggc	gca	act	tct	gca	cag	gct	atg	gca	gga	1075	
Val	Ser	Ile	Gly	Thr	Phe	Gly	Ala	Thr	Ser	Ala	Gln	Ala	Met	Ala	Gly		
	310					315				320					325		
acg	att	ggg	ccc	ttg	att	gaa	att	cca	gta	ctt	gtc	ggc	ttg	gtc	tac	1123	
Thr	Ile	Gly	Pro	Leu	Ile	Glu	Ile	Pro	Val	Leu	Val	Gly	Leu	Val	Tyr		
			330					335						340			
gcc	atg	ctg	tgg	cta	ggc	ccc	aag	ttg	ttc	cca	aat	gac	ccc	acg	ctg	1171	
Ala	Met	Leu	Trp	Leu	Gly	Pro	Lys	Leu	Phe	Pro	Asn	Asp	Pro	Thr	Leu		
			345					350					355				
cca	tca	tca	gct	cgt	tct	acc	agc	caa	atc	atc	aac	tca	tagcgaagga			1220	
Pro	Ser	Ser	Ala	Arg	Ser	Thr	Ser	Gln	Ile	Ile	Asn	Ser					
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atcaacttca	tga															1233	

<210> 122

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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Leu	Asp	Lys	Tyr	Ile	Pro	Leu	Trp	Ile	Ile	Leu	Ala	Met	Ala	Phe	Gly
	20							25					30		

Leu Phe Leu Gly Arg Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala
 35 40 45
 Met Glu Val Gly Gly Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val
 50 55 60
 Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln
 65 70 75 80
 Ile Ala Thr Asp Lys His Leu Met Gly Val Ser Leu Ile Leu Asn Trp
 85 90 95
 Val Val Gly Pro Ala Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro
 100 105 110
 Asp Gln Pro Glu Leu Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg
 115 120 125
 Cys Ile Ala Met Val Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg
 130 135 140
 Glu Ala Thr Ala Val Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala
 145 150 155 160
 Met Phe Gly Ala Leu Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp
 165 170 175
 Leu Gly Leu Pro Thr Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val
 180 185 190
 Thr Ser Val Leu Val Phe Leu Gly Ile Pro Leu Leu Ala Gly Val Phe
 195 200 205
 Ser Arg Ile Ile Gly Glu Lys Ile Lys Gly Arg Glu Trp Tyr Glu Gln
 210 215 220
 Lys Phe Leu Pro Ala Ile Ser Pro Phe Ala Leu Ile Gly Leu Leu Tyr
 225 230 235 240
 Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Gln Ile Val Ser Gln
 245 250 255
 Pro Trp Ala Val Val Arg Leu Ala Ile Pro Leu Val Ile Tyr Phe Val
 260 265 270
 Gly Met Phe Phe Ile Ser Leu Ile Ala Ser Lys Leu Ser Gly Met Asn
 275 280 285
 Tyr Ala Lys Ser Ala Ser Val Ser Phe Thr Ala Ala Gly Asn Asn Phe
 290 295 300
 Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala Thr Ser Ala
 305 310 315 320
 Gln Ala Met Ala Gly Thr Ile Gly Pro Leu Ile Glu Ile Pro Val Leu
 325 330 335

Val Gly Leu Val Tyr Ala Met Leu Trp Leu Gly Pro Lys Leu Phe Pro
 340 345 350

Asn Asp Pro Thr Leu Pro Ser Ser Ala Arg Ser Thr Ser Gln Ile Ile
 355 360 365

Asn Ser
 370

<210> 123

<211> 762

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(739)

<223> RXA02202

<400> 123

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aatctattgg tttccccgta aaatcttcga aaggaagaac atg acc ggg caa gct 115
                                         Met Thr Gly Gln Ala
                                         1 5
gca cca aac ttg cat acc aat att ttg aac cgt atc gca aat gaa ctg 163
Ala Pro Asn Leu His Thr Asn Ile Leu Asn Arg Ile Ala Asn Glu Leu
                        10 15 20
gcg ttg acc tat caa gga gtt ttc tct gca gag act atc aac cgc tat 211
Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu Thr Ile Asn Arg Tyr
                        25 30 35
att ttt gaa tcg tat gtg tcg ttg gcg aga aca gca aaa atc cat acg 259
Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr Ala Lys Ile His Thr
                        40 45 50
cac ctg cca att ttg gca gaa ggt ttt gct aaa gac cgg ctg cac gca 307
His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys Asp Arg Leu His Ala
                        55 60 65
ctt gcg gta gct gaa ggt aag gtg gct tca cct gtg cct cag gtc cta 355
Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro Val Pro Gln Val Leu
                        70 75 80 85
ttt att tgc gtc cac aac gca ggt cgt tca caa att gct tcg gcg ttg 403
Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln Ile Ala Ser Ala Leu
                        90 95 100
ttg tct cac tat gcc ggt agt tct gta gag gta cgt tct gca ggt tct 451
Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val Arg Ser Ala Gly Ser
                        105 110 115
tta cct gct tct gaa att cac cca ctg gtg ttg gaa att ttg tca gag 499
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Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu Glu Il Leu Ser Glu
 120 125 130
 cga gga gtg aac att tct gat gca ttt ccg aaa ccg cta acc gat gat 547
 Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys Pro Leu Thr Asp Asp
 135 140 145
 gtt att cgc gca tct gac tat gtc ata aca atg gga tgt gga gat gtg 595
 Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met Gly Cys Gly Asp Val
 150 155 160 165
 tgc cca atg tat cca gga aag cac tat ctc gat tgg gag ctc gct gat 643
 Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp Trp Glu Leu Ala Asp
 170 175 180
 ccg tca gat gaa ggt gag gac aag ata cag gaa ata att gag gaa att 691
 Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu Ile Ile Glu Glu Ile
 185 190 195
 gac ggt cga atc cgc gag ctt tgg aaa agc att caa tta tcg caa aac 739
 Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile Gln Leu Ser Gln Asn
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 taggcagtca aaggtctggc acc 762

 <210> 124
 <211> 213
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 124
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 Ile Ala Asn Glu Leu Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu
 20 25 30
 Thr Ile Asn Arg Tyr Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr
 35 40 45
 Ala Lys Ile His Thr His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys
 50 55 60
 Asp Arg Leu His Ala Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro
 65 70 75 80
 Val Pro Gln Val Leu Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln
 85 90 95
 Ile Ala Ser Ala Leu Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val
 100 105 110
 Arg Ser Ala Gly Ser Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu
 115 120 125
 Glu Ile Leu Ser Glu Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys

130

135

140

Pro Leu Thr Asp Asp Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met
 145 150 155 160

Gly Cys Gly Asp Val Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp
 165 170 175

Trp Glu Leu Ala Asp Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu
 180 185 190

Ile Ile Glu Glu Ile Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile
 195 200 205

Gln Leu Ser Gln Asn
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<210> 125

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXA02205

<400> 125

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 Val Asn Glu Glu Ile
 1 5

acc ctc cta gcc gca gca gca gat cct gcc gca act gaa aat att ggc 163
 Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala Thr Glu Asn Ile Gly
 10 15 20

tgg gta caa acc att gtg ctc tcc atc gtt caa ggc ctc aca gag ttc 211
 Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln Gly Leu Thr Glu Phe
 25 30 35

ctg ccg atc agc tcc agc gga cac ctc cga atc atc tct gag ctg ttc 259
 Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile Ile Ser Glu Leu Phe
 40 45 50

tgg ggt gcc gat gcc ggc gcg tcc ttt acc gcc gtg gtt cag ctt ggt 307
 Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala Val Val Gln Leu Gly
 55 60 65

acc gaa gcc gca gtg ctg gtg ttt ttt gcc aag gaa atc tgg caa atc 355
 Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys Glu Ile Trp Gln Ile
 70 75 80 85

atc aca ggt tgg ttc gct ggc gta ttc aat aag gaa cgc cgc gga ttt 403
 Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys Glu Arg Arg Gly Phe

90	95	100	
gaa tac cgc atg ggc tgg atg atc att gtt gcc acc att ccc gtc gtg			451
Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala Thr Ile Pro Val Val			
105	110	115	
atc ttg ggt gtg ttg ggc aag gac ctg atc cgt gag gcg ctg cga aat			499
Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg Glu Ala Leu Arg Asn			
120	125	130	
atg tgg atc act gca tcc gtg ctg atc ctg ttc tcc ctg gtg ttc att			547
Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe Ser Leu Val Phe Ile			
135	140	145	
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Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp Tyr Asp Lys Leu Thr			
150	155	160	165
atg aaa gat gcc atc atc atg ggt ctt gca cag tgt ctt gcg ctg atc			643
Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln Cys Leu Ala Leu Ile			
170	175	180	
cct ggc gtg tct cgc tcc ggc ggc acc atc tct gct ggt ttg ttc ctt			691
Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser Ala Gly Leu Phe Leu			
185	190	195	
ggt ctc aag cgt gaa gta gcc acc aag ttc tcc ttc ctg ctg gca atc			739
Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser Phe Leu Leu Ala Ile			
200	205	210	
cct gca gtg ctt ggc tcc ggt ttg tac tcc ctg cct gac gct ttt gcg			787
Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu Pro Asp Ala Phe Ala			
215	220	225	
cca agc tcc gga caa gct gcc tcc ggc cta cag ctc acc gtg ggt acc			835
Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln Leu Thr Val Gly Thr			
230	235	240	245
ctg gtt gcc ttc gta gtt ggc tac att tcc att gcg tgg ctg atg aag			883
Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile Ala Trp Leu Met Lys			
250	255	260	
ttc gtg gca aac cac tcc ttc agc tgg ttt gct gca tac cgt att cct			931
Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala Ala Tyr Arg Ile Pro			
265	270	275	
gca ggt ctg ctc gtg atg ctg ctg ctc gca ctg ggc atg ctc aac cca			979
Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu Gly Met Leu Asn Pro			
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<210> 126

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

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 Gly Leu Thr Glu Phe Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile
 35 40 45
 Ile Ser Glu Leu Phe Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala
 50 55 60
 Val Val Gln Leu Gly Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys
 65 70 75 80
 Glu Ile Trp Gln Ile Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys
 85 90 95
 Glu Arg Arg Gly Phe Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala
 100 105 110
 Thr Ile Pro Val Val Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg
 115 120 125
 Glu Ala Leu Arg Asn Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe
 130 135 140
 Ser Leu Val Phe Ile Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp
 145 150 155 160
 Tyr Asp Lys Leu Thr Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln
 165 170 175
 Cys Leu Ala Leu Ile Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser
 180 185 190
 Ala Gly Leu Phe Leu Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser
 195 200 205
 Phe Leu Leu Ala Ile Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu
 210 215 220
 Pro Asp Ala Phe Ala Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln
 225 230 235 240
 Leu Thr Val Gly Thr Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile
 245 250 255
 Ala Trp Leu Met Lys Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala
 260 265 270
 Ala Tyr Arg Ile Pro Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu
 275 280 285
 Gly Met Leu Asn Pro

<210> 127
<211> 975
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101) .. (952)  
<223> RXA00900
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tagtgatcgc	acgcctggtg	caggggcttg	gcggcggtgc	gtg cgt ggt att gcg	115	
				Val Arg Gly Ile Ala	5	
cgc gcg atc gtg cca gac ctt gaa cgc gga caa aag gct gcg cac gcc	163					
Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln Lys Ala Ala His Ala	10 15 20					
ttt gca ctg ctg atg att att cag gga att gct ccc gtg gta gct ccg	211					
Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala Pro Val Val Ala Pro	25 30 35					
ctc att ggt ggt gtg ctg gtc ggg cct ttt ggc tgg cgg gga att ttc	259					
Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly Trp Arg Gly Ile Phe	40 45 50					
tgg gca ctt gca ctg gtg aat ttt gcg cag ctg ctt gtt gct ttg ctg	307					
Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu Leu Val Ala Leu Leu	55 60 65					
cag att aag gag tcg aag cca gtt gaa gag cgt acc gca gca gga ctt	355					
Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg Thr Ala Ala Gly Leu	70 75 80 85					
ggc gga atg ctg tcc aac tat gtc ttt gtg ctg aag aat cct caa ttt	403					
Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu Lys Asn Pro Gln Phe	90 95 100					
ttg gca tat gta ttc aca ttg ggg ctg tct ttt ggg gcg atg ttc tcc	451					
Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe Gly Ala Met Phe Ser	105 110 115					
tac att tcg gcg tcg ccg ttc gtg ctg cag aat caa atg ggc att ccg	499					
Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn Gln Met Gly Ile Pro	120 125 130					
gta ctg ctg tat tcc att att ttc gga gtg aat gct ttt ggt ttg att	547					
Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn Ala Phe Gly Leu Ile	135 140 145					
gtg ggc gga atg gtc aat agg cga ctt ctg cag cgg att cat cca cac	595					

Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln Arg Ile His Pro His
 150 155 160 165
 cgc atc atg caa act gtg ctg gcc agt ttt act gtg ctg tgt gcg ctt 643
 Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr Val Leu Cys Ala Leu
 170 175 180
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 Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile Pro Leu Phe Leu Leu
 185 190 195
 ctg ctg ttt ctt atc gtt tcc cat att ccg atg gtt atg gct aac gcg 739
 Leu Leu Phe Leu Ile Val Ser His Ile Pro Met Val Met Ala Asn Ala
 200 205 210
 aca gct ctg gga act gaa gtg gtg cga agc agg gcg gga tcg ggt tct 787
 Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg Ala Gly Ser Gly Ser
 215 220 225
 gca att ttg ggt ttc gtg caa ttc acg atg ggt gct ttg gtg agt tca 835
 Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly Ala Leu Val Ser Ser
 230 235 240 245
 ctg gtc gga tta ggc tct gat aag gct ttg act atg gga atc gca atg 883
 Leu Val Gly Leu Ser Asp Lys Ala Leu Thr Met Gly Ile Ala Met
 250 255 260
 act gct tgt gca ctg ctg gcg tgt ggg tgt gcg tac ctg gca ggt cga 931
 Thr Ala Cys Ala Leu Leu Ala Cys Gly Cys Ala Tyr Leu Ala Gly Arg
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 aaa ggt att cca gaa atg aag tagctctagg tggcgtttta agg 975
 Lys Gly Ile Pro Glu Met Lys
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 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 128
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 Lys Ala Ala His Ala Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala
 20 25 30
 Pro Val Val Ala Pro Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly
 35 40 45
 Trp Arg Gly Ile Phe Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu
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 Leu Val Ala Leu Leu Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg
 65 70 75 80

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Met Gln Lys Lys Gln
1 5

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cag ctg agc acc gcc ctg att atg gga ttg gca tta ttg tca gcc agc 163
 Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala Leu Leu Ser Ala Ser
 10 15 20

tcc gcg cta gcg act gat atg tat ttg ccg gca atg cct ggt att gcg 211
 Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met Pro Gly Ile Ala
 25 30 35

gaa gat ttg ggg aca act gca ccg atg gtg cag tta act ctt tct tcc 259
 Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu Thr Leu Ser Ser
 40 45 50

ttt atg gct gga atg gcg att ggc caa ttg atc att ggt cct ttg tcg 307
 Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile Gly Pro Leu Ser
 55 60 65

gat caa ttg gga agg aaa ggc ctg ctc gtt gca ggt gcg gtg gct gcg 355
 Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly Ala Val Ala Ala
 70 75 80 85

ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg ata agc gta tta 403
 Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser Ile Ser Val Leu
 90 95 100

gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt gcg tgc gtg gta 451
 Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly Ala Cys Val Val
 105 110 115

ttg cgc gcg cga tcg tgc cag acc ttg aac gcg gac aaa agg ctg cgc 499
 Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp Lys Arg Leu Arg
 120 125 130

acg cct ttg cac tgc tgatgattat tcagggaatt gct 537
 Thr Pro Leu His Cys
 135

<210> 130

<211> 138

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 130

Met Gln Lys Lys Gln Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala
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Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala
 20 25 30

Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln
 35 40 45

Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile
 50 55 60

Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala
 65 70 75 80

105

110

115

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 120 125

gct 501

<210> 132

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Gly Leu Ala Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met
 1 5 10 15

Tyr Leu Pro Ala Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala
 20 25 30

Pro Met Val Gln Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile
 35 40 45

Gly Gln Leu Ile Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly
 50 55 60

Leu Leu Val Ala Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys
 65 70 75 80

Ala Leu Ala Pro Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln
 85 90 95

Gly Leu Gly Gly Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln
 100 105 110

Thr Leu Asn Ala Asp Lys Arg Leu Arg Thr Pro Leu His Cys
 115 120 125

<210> 133

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> RXA00289

<400> 133

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 Met Ser Thr Thr Thr
 1 5

gcg ccc gaa gca cgg ttt cct gtc gtc cct ttg acc gcc atg agt ttc Ala Pro Glu Ala Arg Phe Pro Val Val Pro Leu Thr Ala Met Ser Phe 10 15 20	163
gcg gca ttt gtt tat gtc acg ttc gag atg ttt gca gtt ggc ctc atc Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe Ala Val Gly Leu Ile 25 30 35	211
aag ccg atg gcc agc gat ctt gga gtg tca gaa tcc agc atc ggc ctg Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu Ser Ser Ile Gly Leu 40 45 50	259
ttg atg act gtg tat gcg act gtc gtt gcc gtg gtg acg atc cct gcc Leu Met Thr Val Tyr Ala Thr Val Val Ala Val Val Thr Ile Pro Ala 55 60 65	307
atg ttg tgg gtt tct cga ttt aac aag cgc aca gtt ttc ctg att act Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr Val Phe Leu Ile Thr 70 75 80 85	355
ctg gca ttt ttg gcc acg ggc att gtt gtt cag gca ctg acc gtt aat Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln Ala Leu Thr Val Asn 90 95 100	403
tat gga atg cta gcc atc ggc cgc act atc gca gca ttg act cac ggg Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala Ala Leu Thr His Gly 105 110 115	451
gtg ttt tgg gca ctt gtt ggg cca atg gca gcg cgt atg tcc cca ggt Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala Arg Met Ser Pro Gly 120 125 130	499
cac act ggt cgt gca gta ggc gtt gtg tgc att gga tca acc atg gcg His Thr Gly Arg Ala Val Gly Val Val Ser Ile Gly Ser Thr Met Ala 135 140 145	547
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gct gta ctc att cca acc gtt cca tca ctg cca cca ctt cca gac acg Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro Pro Leu Pro Asp Thr 185 190 195	691
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ctg gtc att ttc ctt ctc ctt gcc gtc acc ggt gtt ttt gct gcc tac Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly Val Phe Ala Ala Tyr 215 220 225	787
acc tac ctt ggc ctc atc atc gct gaa aca gca ggg gac agc ttc gtg	835

Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala Gly Asp Ser Phe Val 230 235 240 245	
tcc att ggc ttg ttc gcc ttc ggt gca ctc gga ctc att ggc gtg aca Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly Leu Ile Gly Val Thr 250 255 260	883
gtg gca acc cga act gtg gat caa cgc atg ctg cgt gga agt gtt cac Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu Arg Gly Ser Val His 265 270 275	931
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gga tta gag ggc aca cta gcc gta gta gct atc ttc ctt gca gtc acc Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile Phe Leu Ala Val Thr 295 300 305	1027
gtg ttt ggt gga gca tac ggc gct ctc cca acc ctg gga acc acc atc Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr Leu Gly Thr Thr Ile 310 315 320 325	1075
ttc ctc cat gcg ggt cgc gac cac cca gat act gca tcc tcc att tat Phe Leu His Ala Gly Arg Asp His Pro Asp Thr Ala Ser Ser Ile Tyr 330 335 340	1123
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gga ctg tca ttg gct tcc acg ttg gcc ttg gcg ctg tgg tcc cgc ccg Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala Leu Trp Ser Arg Pro 375 380 385	1267
cta ctg aag tagcagccca aattcagccc act Leu Leu Lys 390	1299

<210> 134

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

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Thr Ala Met Ser Phe Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe
20 25 30

Ala Val Gly Leu Ile Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu

35	40	45
Ser Ser Ile Gly Leu Leu Met Thr Val Tyr Ala Thr Val Val Ala Val 50 55 60		
Val Thr Ile Pro Ala Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr 65 70 75 80		
Val Phe Leu Ile Thr Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln 85 90 95		
Ala Leu Thr Val Asn Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala 100 105 110		
Ala Leu Thr His Gly Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala 115 120 125		
Arg Met Ser Pro Gly His Thr Gly Arg Ala Val Gly Val Val Ser Ile 130 135 140		
Gly Ser Thr Met Ala Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile 145 150 155 160		
Gly Glu Leu Ile Gly Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu 165 170 175		
Thr Ile Ala Ala Val Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro 180 185 190		
Pro Leu Pro Asp Thr Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro 195 200 205		
Trp Gly Leu Ile Ser Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly 210 215 220		
Val Phe Ala Ala Tyr Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala 225 230 235 240		
Gly Asp Ser Phe Val Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly 245 250 255		
Leu Ile Gly Val Thr Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu 260 265 270		
Arg Gly Ser Val His Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu 275 280 285		
Gly Gln Ile Ala Phe Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile 290 295 300		
Phe Leu Ala Val Thr Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr 305 310 315 320		
Leu Gly Thr Thr Ile Phe Leu His Ala Gly Arg Asp His Pro Asp Thr 325 330 335		
Ala Ser Ser Ile Tyr Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly		

340

345

350

Ala Ala Leu Gly Ala Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr
 355 360 365

Leu Trp Ile Met Ala Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala
 370 375 380

Leu Trp Ser Arg Pro Leu Leu Lys
 385 390

<210> 135

<211> 420

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(397)

<223> RXN01984

<400> 135

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 Met His Glu Ser Gly
 1 5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
 Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
 10 15 20

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
 Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
 25 30 35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
 Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
 40 45 50

ggg ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307
 Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
 55 60 65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac 355
 Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
 70 75 80 85

atc atc acc atc tac gcc ctc gcg tgg ttg tgg gtg ccc cgc 397
 Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp Val Pro Arg
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<210> 136

<211> 99
 <212> PRT
 <213> Corynebacterium glutamicum

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 Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
 35 40 45
 Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
 50 55 60
 Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65 70 75 80
 Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp
 85 90 95
 Val Pro Arg

<210> 137
 <211> 379
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(379)
 <223> FRXA01984

<400> 137
 aggaaatgtc tcacgtcaca accttttgaa aggtgggctaa gtacgcacat ttgttgtctg 60
 caatagtgcc ggtgagggag ctgtccgata ttgtgcttac atg cac gaa tct gga 115
 Met His Glu Ser Gly
 1 5
 aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
 Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
 10 15 20
 ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
 Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
 25 30 35
 gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
 Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
 40 45 50
 ggt ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307

Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
 55 60 65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac 355
 Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
 70 75 80 85

atc atc acc atc tac gcc ctc gcg 379
 Ile Ile Thr Ile Tyr Ala Leu Ala
 90

<210> 138

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
 1 5 10 15

Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
 20 25 30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
 35 40 45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
 50 55 60

Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65 70 75 80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala
 85 90

<210> 139

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(712)

<223> RXA00109

<400> 139

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cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag 115
 Val Ala Ser Glu Lys
 1 5

aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt 163
 Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Gly Val Leu Gly Val
 10 15 20

ggc gcg atg tcg atg ctc gtg gct ccg cag gct gct gcc cat gat gtg 211
 Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val
 25 30 35

gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg 259
 Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro
 40 45 50

gag acc att gag ttg gag ttt tcc ggt att cct cag gat ctg ttc aca 307
 Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr
 55 60 65

aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga 355
 Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly
 70 75 80 85

act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat 403
 Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp
 90 95 100

gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct 451
 Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser
 105 110 115

tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc 499
 Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly
 120 125 130

tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca 547
 Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu Thr Thr Thr Glu Ser
 135 140 145

gca gca acc act gac acc tca gag acc acc gaa gca gag aca act gaa 595
 Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu
 150 155 160 165

act gct gat gaa act tct gga att cct gcg ccg tgg aat tgg gtt ttg 643
 Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu
 170 175 180

agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att 691
 Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile
 185 190 195

gca aag aat cgt aac cag aaa taagagggtt tattcaccat gaa 735
 Ala Lys Asn Arg Asn Gln Lys
 200

<210> 140

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala

1	5	10	15
Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala	20	25	30
Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val	35	40	45
Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro	50	55	60
Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu	65	70	75
Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr	85	90	95
Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly	100	105	110
Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser	115	120	125
Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu	130	135	140
Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu	145	150	155
Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro	165	170	175
Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala	180	185	190
Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys	195	200	

<210> 141

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(712)

<223> RXA00109

<400> 141

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cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag 115
 Val Ala Ser Glu Lys
 1 5

aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt 163

Asn	Leu	Lys	Leu	Arg	Thr	Leu	Ala	Ala	Ala	Ala	Gly	Val	Leu	Gly	Val		
				10						15				20			
ggc	gcg	atg	tcg	atg	ctc	gtg	gct	ccg	cag	gct	gct	gcc	cat	gat	gtg	211	
Gly	Ala	Met	Ser	Met	Leu	Val	Ala	Pro	Gln	Ala	Ala	Ala	His	Asp	Val		
			25					30					35				
gtg	gtg	gat	tct	aat	cct	gaa	aat	ggc	agt	gtc	gtt	gat	gag	ttc	ccg	259	
Val	Val	Asp	Ser	Asn	Pro	Glu	Asn	Gly	Ser	Val	Val	Asp	Glu	Phe	Pro		
		40					45					50					
gag	acc	att	gag	ttg	gag	ttt	tcc	ggg	att	cct	cag	gat	ctg	ttc	aca	307	
Glu	Thr	Ile	Glu	Leu	Glu	Phe	Ser	Gly	Ile	Pro	Gln	Asp	Leu	Phe	Thr		
	55					60					65						
aca	gtt	gca	ttg	agc	aat	gcg	gat	tcc	gga	gag	gtg	tta	act	tct	gga	355	
Thr	Val	Ala	Leu	Ser	Asn	Ala	Asp	Ser	Gly	Glu	Val	Leu	Thr	Ser	Gly		
	70				75					80					85		
act	cct	cag	ctt	gag	ggg	cag	cac	ttg	agc	tat	gaa	gtg	cca	tct	gat	403	
Thr	Pro	Gln	Leu	Glu	Gly	Gln	His	Leu	Ser	Tyr	Glu	Val	Pro	Ser	Asp		
			90						95					100			
gtg	cag	acg	gga	gct	ggg	aac	tac	att	ttg	ggg	ttc	cag	atc	act	tct	451	
Val	Gln	Thr	Gly	Ala	Gly	Asn	Tyr	Ile	Leu	Gly	Phe	Gln	Ile	Thr	Ser		
			105					110					115				
tct	gat	ggg	cac	gct	act	aaa	ggg	tca	atc	tct	ttt	gag	gtg	aca	ggc	499	
Ser	Asp	Gly	His	Ala	Thr	Lys	Gly	Ser	Ile	Ser	Phe	Glu	Val	Thr	Gly		
		120					125					130					
tct	gct	gaa	acg	aca	aca	gag	aca	aca	gca	gag	acg	aca	act	gag	tca	547	
Ser	Ala	Glu	Thr	Thr	Thr	Glu	Thr	Thr	Ala	Glu	Thr	Thr	Thr	Glu	Ser		
	135					140					145						
gca	gca	acc	act	gac	acc	tca	gag	acc	acc	gaa	gca	gag	aca	act	gaa	595	
Ala	Ala	Thr	Thr	Asp	Thr	Ser	Glu	Thr	Thr	Glu	Ala	Glu	Thr	Thr	Glu		
	150				155					160					165		
act	gct	gat	gaa	act	tct	gga	att	cct	gcg	ccg	tgg	aat	tgg	gtt	ttg	643	
Thr	Ala	Asp	Glu	Thr	Ser	Gly	Ile	Pro	Ala	Pro	Trp	Asn	Trp	Val	Leu		
			170					175						180			
agc	atc	gtg	gcg	gtg	ctt	gtt	gtt	gca	agt	gcc	atc	gtc	atg	atg	att	691	
Ser	Ile	Val	Ala	Val	Leu	Val	Val	Ala	Ser	Ala	Ile	Val	Met	Met	Ile		
			185					190					195				
gca	aag	aat	cgt	aac	cag	aaa	taagagggtt	tattcaccat	gaa							735	
Ala	Lys	Asn	Arg	Asn	Gln	Lys											
		200															

<210> 142

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala
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Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala
 20 25 30

Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
 35 40 45

Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
 50 55 60

Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
 65 70 75 80

Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
 85 90 95

Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
 100 105 110

Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
 115 120 125

Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
 130 135 140

Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
 145 150 155 160

Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
 165 170 175

Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
 180 185 190

Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
 195 200

<210> 143

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA00996

<400> 143

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acctctatct tgcacctgat ctggcgtaga ctcataagtt atg agc acc gta acg 115
 Met Ser Thr Val Thr
 1 5

gca gtg cag gtc aac ggc cta aaa gtt tcc ata tcg tcc ggt ttt tca	163
Ala Val Gln Val Asn Gly Leu Lys Val Ser Il Ser Ser Gly Phe Ser	
10 15 20	
cgc aag aaa aca aaa acg atc ttg cat gat ctc gat ttc acc gta gag	211
Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu Asp Phe Thr Val Glu	
25 30 35	
acc gga aag atc acg gga ttg ctg ggg cca tcg ggc agc ggc aag aca	259
Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser Gly Ser Gly Lys Thr	
40 45 50	
act ttg atg cgc gcg att gtg gga gtg caa aac ttc gac ggc acc ctt	307
Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn Phe Asp Gly Thr Leu	
55 60 65	
gag gtg ttt gat cag ccc gca ggt gct gcc tct ctg cgc ggg aaa atc	355
Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser Leu Arg Gly Lys Ile	
70 75 80 85	
ggc tat gtc acc caa aac gcc agc gta tat cac gat ctg tcg gtg ata	403
Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His Asp Leu Ser Val Ile	
90 95 100	
gaa aac ctc aag tat ttc ggg gct ctg gct aaa gga acc tcc act cca	451
Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys Gly Thr Ser Thr Pro	
105 110 115	
cgc acc ccg gaa aag att ctg gag gtc tta gac atc gca gat ctt gct	499
Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp Ile Ala Asp Leu Ala	
120 125 130	
caa cgc caa gta tca aca cta tct ggt ggg cag cgc ggc cga gtc tcc	547
Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln Arg Gly Arg Val Ser	
135 140 145	
ctt gga tgt gcg ctt att gcc tca cca gaa ctc ttg gtg atg gat gag	595
Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu Leu Val Met Asp Glu	
150 155 160 165	
cca acc gtg ggt ttg gat ccc att acc cgg caa gca ctg tgg gaa gag	643
Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln Ala Leu Trp Glu Glu	
170 175 180	
ttc acc acc atc gca aaa gca ggt gct gga gtg gtt atc tcc agt cac	691
Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val Val Ile Ser Ser His	
185 190 195	
gtg ttg gag gaa gcc gcg cgg tgc gac aac ctc att ttg ttg cgt gat	739
Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu Ile Leu Leu Arg Asp	
200 205 210	
ggt cgg atc atc tgg agg gga aca ccc aca cgc ctt cta gaa gat aca	787
Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg Leu Leu Glu Asp Thr	
215 220 225	

ggc aaa agc tca tac gaa gat gct ttc ttg gct gcc att gac ggg gta 835
 Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala Ala Ile Asp Gly Val
 230 235 240 245

agg tca tgaaccctca ctatctgctt gcc 864
 Arg Ser

<210> 144

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Ser Thr Val Thr Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile
 1 5 10 15

Ser Ser Gly Phe Ser Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu
 20 25 30

Asp Phe Thr Val Glu Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser
 35 40 45

Gly Ser Gly Lys Thr Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn
 50 55 60

Phe Asp Gly Thr Leu Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser
 65 70 75 80

Leu Arg Gly Lys Ile Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His
 85 90 95

Asp Leu Ser Val Ile Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys
 100 105 110

Gly Thr Ser Thr Pro Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp
 115 120 125

Ile Ala Asp Leu Ala Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln
 130 135 140

Arg Gly Arg Val Ser Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu
 145 150 155 160

Leu Val Met Asp Glu Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln
 165 170 175

Ala Leu Trp Glu Glu Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val
 180 185 190

Val Ile Ser Ser His Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu
 195 200 205

Ile Leu Leu Arg Asp Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg
 210 215 220

Leu Leu Glu Asp Thr Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala
 225 230 235 240

Ala Ile Asp Gly Val Arg Ser
 245

<210> 145

<211> 2463

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2440)

<223> RXN00829

<400> 145

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caagcgcgaa caggcctatg caaacggtac gatatgacac atg caa aaa gct gat 115
 Met Gln Lys Ala Asp
 1 5

tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa 163
 Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
 10 15 20

aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt 211
 Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly
 25 30 35

gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg 259
 Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala
 40 45 50

gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt 307
 Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly
 55 60 65

ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc 355
 Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile
 70 75 80 85

acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg 403
 Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg
 90 95 100

tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg 451
 Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu
 105 110 115

ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc 499
 Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser
 120 125 130

ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag 547

Phe	Asn	Val	Pro	Ser	Val	Ser	Ala	Ser	Gly	Ala	Ile	Thr	Val	Glu	Lys	
135						140					145					
ggc	gga	aac	acc	aag	cgg	gag	aaa	gct	acc	ttc	aaa	cgc	acg	ggt	ggc	595
Gly	Gly	Asn	Thr	Lys	Arg	Glu	Lys	Ala	Thr	Phe	Lys	Arg	Thr	Gly	Gly	
150					155					160					165	
atg	tgc	cca	gcg	tgc	gag	ggc	atg	ggc	agg	gcc	tca	gac	atc	gac	ctc	643
Met	Cys	Pro	Ala	Cys	Glu	Gly	Met	Gly	Arg	Ala	Ser	Asp	Ile	Asp	Leu	
				170					175					180		
aaa	gag	ctt	ttc	gac	gcc	tcc	ctc	tcc	ctc	aac	gac	ggc	gcc	ctg	acc	691
Lys	Glu	Leu	Phe	Asp	Ala	Ser	Leu	Ser	Leu	Asn	Asp	Gly	Ala	Leu	Thr	
			185					190					195			
atc	ccc	ggt	tac	acc	cca	ggt	gga	tgg	agt	tat	cgg	atg	tat	tca	gaa	739
Ile	Pro	Gly	Tyr	Thr	Pro	Gly	Gly	Trp	Ser	Tyr	Arg	Met	Tyr	Ser	Glu	
		200					205					210				
tcg	ggc	ctt	ttt	gat	gct	gcc	aag	ccg	att	aag	gat	ttc	acc	gag	gaa	787
Ser	Gly	Leu	Phe	Asp	Ala	Ala	Lys	Pro	Ile	Lys	Asp	Phe	Thr	Glu	Glu	
	215					220					225					
gaa	cgc	cac	aac	ttc	ctt	tat	ctt	gag	ccc	acc	aag	atg	aag	atc	gct	835
Glu	Arg	His	Asn	Phe	Leu	Tyr	Leu	Glu	Pro	Thr	Lys	Met	Lys	Ile	Ala	
230					235					240					245	
ggc	atc	aac	atg	acc	tat	gag	ggt	ctt	atc	ccc	cgc	att	cag	aaa	tcc	883
Gly	Ile	Asn	Met	Thr	Tyr	Glu	Gly	Leu	Ile	Pro	Arg	Ile	Gln	Lys	Ser	
				250					255					260		
atg	ttg	tct	aag	gat	cgc	gaa	ggc	atg	cag	aag	cat	att	cgt	gcg	ttc	931
Met	Leu	Ser	Lys	Asp	Arg	Glu	Gly	Met	Gln	Lys	His	Ile	Arg	Ala	Phe	
			265					270					275			
gtg	gat	cga	gcg	gtt	acc	ttc	att	cct	tgc	cct	gcg	tgt	ggt	gga	act	979
Val	Asp	Arg	Ala	Val	Thr	Phe	Ile	Pro	Cys	Pro	Ala	Cys	Gly	Gly	Thr	
		280					285					290				
cga	tta	gcg	cca	cat	gcc	ttg	gag	tcc	aag	atc	aat	ggc	aaa	aac	atc	1027
Arg	Leu	Ala	Pro	His	Ala	Leu	Glu	Ser	Lys	Ile	Asn	Gly	Lys	Asn	Ile	
	295					300					305					
gct	gag	ttg	tgc	gcg	atg	gag	gtc	cgt	gat	ttg	gcc	aag	tgg	atc	aaa	1075
Ala	Glu	Leu	Cys	Ala	Met	Glu	Val	Arg	Asp	Leu	Ala	Lys	Trp	Ile	Lys	
310					315					320					325	
acg	gtg	gaa	gcc	ccc	tgc	gtt	gct	ccc	ctg	ctc	acc	gca	ctg	act	gaa	1123
Thr	Val	Glu	Ala	Pro	Ser	Val	Ala	Pro	Leu	Leu	Thr	Ala	Leu	Thr	Glu	
				330					335					340		
acc	ctg	gat	aac	ttc	gtg	gag	atc	ggt	ttg	ggc	tat	atc	caa	ctc	gat	1171
Thr	Leu	Asp	Asn	Phe	Val	Glu	Ile	Gly	Leu	Gly	Tyr	Ile	Gln	Leu	Asp	
			345					350					355			
cgc	ccc	gct	ggc	acg	ttg	tct	ggt	ggt	gag	gca	cag	cgc	acc	aag	atg	1219
Arg	Pro	Ala	Gly	Thr	Leu	Ser	Gly	Gly	Glu	Ala	Gln	Arg	Thr	Lys	Met	

360	365	370	
atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp 375 380 385			1267
gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys 390 395 400 405			1315
ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu 410 415 420			1363
cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly 425 430 435			1411
cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val 440 445 450			1459
gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp 455 460 465			1507
cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu 470 475 480 485			1555
atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile 490 495 500			1603
ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys 505 510 515			1651
tcc tcg ttg att cat gag att ccg cgt gat gag tcg gtt gtg ttt gtc Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu Ser Val Val Phe Val 520 525 530			1699
gat caa acc gca atc cac ggt tct aat cgt tcc aat cct gcg aca tat Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser Asn Pro Ala Thr Tyr 535 540 545			1747
aca ggc atg ctg gat tcg att cgc aag gct ttt gcc aag gcc aat gat Thr Gly Met Leu Asp Ser Ile Arg Lys Ala Phe Ala Lys Ala Asn Asp 550 555 560 565			1795
gtg aaa ccg gcg ctg ttc tcc ccc aat tct gaa ggc gcg tgc cca aac Val Lys Pro Ala Leu Phe Ser Pro Asn Ser Glu Gly Ala Cys Pro Asn 570 575 580			1843
tgt aag ggc gcc ggc tcg gtc tat gtc gat ttg ggc atg atg gct ggg Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu Gly Met Met Ala Gly 585 590 595			1891

gta tct tcg ccg tgt gag gtg tgc gag ggc aag cgt ttt gat gag tcc 1939
 Val S r Ser Pro Cys Glu Val Cys Glu Gly Lys Arg Phe Asp Glu Ser
 600 605 610

gtg ttg gac tac cac ttt ggt ggc aag gac atc gca gac. gtg ttg ggg 1987
 Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile Ala Asp Val Leu Gly
 615 620 625

ctg tcg gct gcc aat gcg tat gag ttt ttc gcg gcg aaa gat tca aag 2035
 Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala Ala Lys Asp Ser Lys
 630 635 640 645

att ttg cct gcg gca aag atc gca aag agg ctt gtc gac gtc ggc ctc 2083
 Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu Val Asp Val Gly Leu
 650 655 660

ggc tac atc acc ctc ggc cag ccg ctc acc acg ttg tcc ggc ggt gaa 2131
 Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr Leu Ser Gly Gly Glu
 665 670 675

cgc cag cgt ttg aag ctc gcc acc cac atg gca gac aag gcc acc acc 2179
 Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala Asp Lys Ala Thr Thr
 680 685 690

ttt att ttg gat gag ccc acc aca ggc ctg cac ctc gct gat gtg aaa 2227
 Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys
 695 700 705

acc ttg ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc 2275
 Thr Leu Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val
 710 715 720 725

atc gtc atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc 2323
 Ile Val Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile
 730 735 740

att gat gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc 2371
 Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe
 745 750 755

gag ggc agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc 2419
 Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg
 760 765 770

cac ctt aaa gct tat gta gat tagtttctta tggaaaaccc tgg 2463
 His Leu Lys Ala Tyr Val Asp
 775 780

<210> 146

<211> 780

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe	35	40	45
Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser	50	55	60
Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp	65	70	75
His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met	85	90	95
Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala	100	105	110
Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly	115	120	125
Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala	130	135	140
Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe	145	150	155
Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala	165	170	175
Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn	180	185	190
Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr	195	200	205
Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys	210	215	220
Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr	225	230	235
Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro	245	250	255
Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys	260	265	270
His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro	275	280	285
Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile	290	295	300
Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu			

305	310	315	320
Ala Lys Trp Ile	Lys Thr Val Glu Ala	Pro Ser Val Ala	Pro Leu Leu
	325	330	335
Thr Ala Leu Thr	Glu Thr Leu Asp Asn	Phe Val Glu Ile	Gly Leu Gly
	340	345	350
Tyr Ile Gln Leu	Asp Arg Pro Ala	Gly Thr Leu Ser	Gly Gly Glu Ala
	355	360	365
Gln Arg Thr Lys	Met Ile Arg His	Leu Gly Ser Ala	Leu Thr Asp Val
	370	375	380
Thr Tyr Val Phe	Asp Glu Pro Thr	Ala Gly Leu His	Ala Tyr Asp Ile
	385	390	395
Glu Arg Met Asn	Lys Leu Leu Leu	Asp Leu Arg Asp	Lys Gly Asn Thr
	405	410	415
Val Leu Val Val	Glu His Lys Pro	Glu Thr Ile Ala	Ile Ala Asp His
	420	425	430
Val Val Asp Leu	Gly Pro Gly Ala	Gly Ala Gly Gly	Gly Glu Ile Arg
	435	440	445
Phe Glu Gly Ser	Val Asp Lys Leu	Lys Asp Ser Asp	Thr Val Thr Gly
	450	455	460
Leu His Phe Asn	Asp Arg Ala Ser	Leu Lys Glu Ser	Val Arg Ala Pro
	465	470	475
His Gly Ala Leu	Glu Ile Arg Gly	Ala Asp Arg Asn	Asn Leu Asn Asn
	485	490	495
Val Asp Val Asp	Ile Pro Leu Gly	Val Phe Thr Ala	Ile Ser Gly Val
	500	505	510
Ala Gly Ser Gly	Lys Ser Ser Leu	Ile His Glu Ile	Pro Arg Asp Glu
	515	520	525
Ser Val Val Phe	Val Asp Gln Thr	Ala Ile His Gly	Ser Asn Arg Ser
	530	535	540
Asn Pro Ala Thr	Tyr Thr Gly Met	Leu Asp Ser Ile	Arg Lys Ala Phe
	545	550	555
Ala Lys Ala Asn	Asp Val Lys Pro	Ala Leu Phe Ser	Pro Asn Ser Glu
	565	570	575
Gly Ala Cys Pro	Asn Cys Lys Gly	Ala Gly Ser Val	Tyr Val Asp Leu
	580	585	590
Gly Met Met Ala	Gly Val Ser Ser	Pro Cys Glu Val	Cys Glu Gly Lys
	595	600	605
Arg Phe Asp Glu	Ser Val Leu Asp	Tyr His Phe Gly	Gly Lys Asp Ile

610	615	620
Ala Asp Val Leu Gly Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala 625 630 635 640		
Ala Lys Asp Ser Lys Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu 645 650 655		
Val Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr 660 665 670		
Leu Ser Gly Gly Glu Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala 675 680 685		
Asp Lys Ala Thr Thr Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His 690 695 700		
Leu Ala Asp Val Lys Thr Leu Leu Asp Leu Phe Asp Gln Leu Val Asp 705 710 715 720		
Asp Gly Lys Ser Val Ile Val Ile Glu His His Leu Gly Val Leu Ala 725 730 735		
His Ala Asp His Ile Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly 740 745 750		
Gly Ser Ile Val Phe Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp 755 760 765		
Thr Pro Thr Gly Arg His Leu Lys Ala Tyr Val Asp 770 775 780		

<210> 147

<211> 278

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(255)

<223> FRXA00829

<400> 147

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Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys Thr Leu	
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ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc atc gtc	96
Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val	
20 25 30	
atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc att gat	144
Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp	
35 40 45	
gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc gag ggc	192

Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60
 agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc cac ctt 240
 Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
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 aaa gct tat gta gat tagtttctta tggaaaaccc tgg 278
 Lys Ala Tyr Val Asp
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<210> 148
 <211> 85
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 148
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 20 25 30
 Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
 35 40 45
 Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60
 Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
 65 70 75 80
 Lys Ala Tyr Val Asp
 85

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 <211> 1663
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1663)
 <223> FRXA00834

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 Met Gln Lys Ala Asp
 1 5
 tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa 163
 Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
 10 15 20

aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt	211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly	
25 30 35	
gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg	259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala	
40 45 50	
gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt	307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly	
55 60 65	
ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc	355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile	
70 75 80 85	
acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg	403
Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg	
90 95 100	
tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg	451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu	
105 110 115	
ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc	499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser	
120 125 130	
ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag	547
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys	
135 140 145	
ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc	595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly	
150 155 160 165	
atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc	643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu	
170 175 180	
aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc	691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr	
185 190 195	
atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa	739
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu	
200 205 210	
tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa	787
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu	
215 220 225	
gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct	835
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala	
230 235 240 245	

ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc	883
Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser	
250 255 260	
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Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe	
265 270 275	
gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act	979
Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr	
280 285 290	
cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc	1027
Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile	
295 300 305	
gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa	1075
Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys	
310 315 320 325	
acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa	1123
Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu	
330 335 340	
acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat	1171
Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp	
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cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg	1219
Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met	
360 365 370	
atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat	1267
Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp	
375 380 385	
gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag	1315
Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys	
390 395 400 405	
ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag	1363
Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu	
410 415 420	
cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg	1411
His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly	
425 430 435	
cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc	1459
Pro Gly Ala Gly Ala Gly Gly Glu Ile Arg Phe Glu Gly Ser Val	
440 445 450	
gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac	1507
Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp	
455 460 465	
cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag	1555

Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
 470 475 480 485

atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att 1603
 Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
 490 495 500

ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag 1651
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 505 510 515

tcc tcg ttg att 1663
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<210> 150
 <211> 521
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 150
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Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe
 35 40 45

Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser
 50 55 60

Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp
 65 70 75 80

His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met
 85 90 95

Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala
 100 105 110

Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly
 115 120 125

Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala
 130 135 140

Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe
 145 150 155 160

Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
 165 170 175

Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
 180 185 190

Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
 195 200 205
 Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
 210 215 220
 Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
 225 230 235 240
 Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
 245 250 255
 Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
 260 265 270
 His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
 275 280 285
 Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
 290 295 300
 Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu
 305 310 315 320
 Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
 325 330 335
 Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
 340 345 350
 Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
 355 360 365
 Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
 370 375 380
 Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
 385 390 395 400
 Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
 405 410 415
 Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
 420 425 430
 Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg
 435 440 445
 Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
 450 455 460
 Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro
 465 470 475 480
 His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
 485 490 495

Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
 500 505 510

Ala Gly Ser Gly Lys S r Ser Leu Ile
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<210> 151

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA00995

<400> 151

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                                         Met Asn Pro His Tyr
                                         1 5

ctg ctt gcc acg gtc aaa cga gtc ctg ctg cag ctg aaa gcc gat aaa 163
Leu Leu Ala Thr Val Lys Arg Val Leu Leu Gln Leu Lys Ala Asp Lys
                        10 15 20

cgt tcc atc gcg ctg att ctt cta gca ccc gtg gcg ttg atg tcg ctg 211
Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val Ala Leu Met Ser Leu
                        25 30 35

ttt tat tac atg tat tcc tcc aca ccg gca ggc acc cag ctg ttt aag 259
Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly Thr Gln Leu Phe Lys
                        40 45 50

acc att tcc acg gtc atg atc gca gtg ttc ccc ttg atg ctc atg ttt 307
Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro Leu Met Leu Met Phe
                        55 60 65

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Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg Asn Ala Gly Thr Leu
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Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val Asp Leu Ile Gly Gly
                        90 95 100

tac ggg gtg gcc ttc ggc atc atg gcg gtg gcg caa tct ttg ctc atg 451
Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala Gln Ser Leu Leu Met
                        105 110 115

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Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu Thr Glu Ser Glu Trp
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tgg att tct acg ctc att gct gcg atc acc ggt ctt atc gga gtg tct 547
 Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly Leu Ile Gly Val Ser
 135 140 145

 ctt ggc ctg ttg agc tct gcg ttt gcc agc act gag ttc caa gct atc 595
 Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr Glu Phe Gln Ala Ile
 150 155 160 165

 caa acg ctg ccg ttg ctt att ttg ccc cag ttc cta ttg tgc ggt ttg 643
 Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe Leu Leu Cys Gly Leu
 170 175-- 180

 ctg atc cca cgg gat gat ctg ccg gat gtg ttg cgc tgg gtt tct aat 691
 Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu Arg Trp Val Ser Asn
 185 190 195

 gtg ttg ccg ctg tcc tat gca gtt gat gca gcg ctt gag gcc tca cgg 739
 Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala Leu Glu Ala Ser Arg
 200 205 210

 acg gga atc gga cag caa gta gtg gtc aac att gcc atc tgc gcc gcg 787
 Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile Ala Ile Cys Ala Ala
 215 220 225

 ttt gcc gtg agc ttc ctg ctg gtg gcg gcg cta tcg atg ccg aga atg 835
 Phe Ala Val Ser Phe Leu Leu Val Ala Ala Leu Ser Met Pro Arg Met
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 Thr Arg

<210> 152

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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 20 25 30

Ala Leu Met Ser Leu Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly
 35 40 45

Thr Gln Leu Phe Lys Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro
 50 55 60

Leu Met Leu Met Phe Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg
 65 70 75 80

Asn Ala Gly Thr Leu Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val
 85 90 95

Asp Leu Ile Gly Gly Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala
 100 105 110
 Gln Ser Leu Leu Met Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu
 115 120 125
 Thr Glu Ser Glu Trp Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly
 130 135 140
 Leu Ile Gly Val Ser Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr
 145 150 155 160
 Glu Phe Gln Ala Ile Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe
 165 170 175
 Leu Leu Cys Gly Leu Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu
 180 185 190
 Arg Trp Val Ser Asn Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala
 195 200 205
 Leu Glu Ala Ser Arg Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile
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 Ser Met Pro Arg Met Thr Arg
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<210> 153
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1330)
 <223> RXN00803

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 Met Gly Val Ser Ala
 1 5
 ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
 Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
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 Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
 25 30 35
 gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259

Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser	
40	45 50
aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg	307
Asn Leu Phe Ile Asp Leu Leu Val Phe Tyr Ala Ile Gly Val Ala	
55	60 65
gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt	355
Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg	
70	75 80 85
gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg	403
Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu	
	90 95 100
att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg	451
Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val	
	105 110 115
ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg	499
Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp	
	120 125 130
att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt	547
Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser	
	135 140 145
gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc	595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu	
150	155 160 165
ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca cta cct gga	643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Leu Pro Gly	
	170 175 180
cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg	691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro	
	185 190 195
ttg ctt att aca gcg ccg gaa act cgt caa tca gcg cac ctg aaa act	739
Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser Ala His Leu Lys Thr	
	200 205 210
aag gga tca ttc tgg tca gat gtg ctt gtg cca tct gca cta gac aag	787
Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro Ser Ala Leu Asp Lys	
	215 220 225
cga ttc ttg ttt gtg gtt gct cca att gga ccg tgg gtt ttc ggt gcg	835
Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro Trp Val Phe Gly Ala	
230	235 240 245
gcc ttc act gcc tac gca gtt ttg ccg tcg cag ctg cgt gac atg gtt	883
Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln Leu Arg Asp Met Val	
	250 255 260
tct gca ccc gtt gcg tat tct gcg ctg atc gct ttg gtt acc tta ggt	931
Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala Leu Val Thr Leu Gly	

265	270	275	
tct gga ttt ggt atc caa caa ttc ggt cct caa atc atg ggc acc tct			979
Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln Ile Met Gly Thr Ser			
280	285	290	
aaa act cgc ggg ccg att ttg gcc atg ttc gtc aca gtc atc ggc atg			1027
Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val Thr Val Ile Gly Met			
295	300	305	
atc ggc gcg gtg atc gtg gtg atg aac cct cat cca tgg tgg gcg cta			1075
Ile Gly Ala Val Ile Val Val Met Asn Pro His Pro Trp Trp Ala Leu			
310	315	320	325
gtt ggc tgc atg gcc ctc ggc ctg tct tat ggc ctg tgt atg ttc atg			1123
Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly Leu Cys Met Phe Met			
330	335	340	
ggg ttg gcg gaa act caa aac att gct cca cct att gat atg gca ggc			1171
Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro Ile Asp Met Ala Gly			
345	350	355	
ctg acg ggt att ttc tac tgc ctg acg tac gta ggt atg gtc ttt cca			1219
Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val Gly Met Val Phe Pro			
360	365	370	
gcc ttg atg acc tgg ttg aat caa tgg ctc agt tac ccg ttc atg ctg			1267
Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser Tyr Pro Phe Met Leu			
375	380	385	
ggc ttt ggt gcg gtg atg gca act att tgt ctg atc att gtg agt ttt			1315
Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu Ile Ile Val Ser Phe			
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agt gca cgc cga ttc tgagaaacaa ctaaagttag cca			1353
Ser Ala Arg Arg Phe			
410			

<210> 154

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

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Ala	Gln	Arg	Lys	Val	Trp	Leu	Ala	Val	Ala	Leu	Ser	Val	Phe	Thr	Val
			20					25					30		

Ala	Trp	Gly	Gly	Asn	Glu	Phe	Thr	Pro	Leu	Leu	Val	Phe	Tyr	Arg	Gly
		35					40					45			

Glu	Gly	Phe	Phe	Ser	Asn	Leu	Phe	Ile	Asp	Leu	Leu	Val	Phe	Tyr
	50					55					60			

Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65 70 75 80
 Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
 85 90 95
 Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
 100 105 110
 Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
 115 120 125
 Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
 130 135 140
 Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
 145 150 155 160
 Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
 165 170 175
 Leu Pro Leu Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
 180 185 190
 Leu Ile Leu Phe Pro Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser
 195 200 205
 Ala His Leu Lys Thr Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro
 210 215 220
 Ser Ala Leu Asp Lys Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro
 225 230 235 240
 Trp Val Phe Gly Ala Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln
 245 250 255
 Leu Arg Asp Met Val Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala
 260 265 270
 Leu Val Thr Leu Gly Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln
 275 280 285
 Ile Met Gly Thr Ser Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val
 290 295 300
 Thr Val Ile Gly Met Ile Gly Ala Val Ile Val Val Met Asn Pro His
 305 310 315 320
 Pro Trp Trp Ala Leu Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly
 325 330 335
 Leu Cys Met Phe Met Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro
 340 345 350
 Ile Asp Met Ala Gly Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val
 355 360 365

Gly M t Val Phe Pro Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser
 370 375 380

Tyr Pro Phe Met Leu Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu
 385 390 395 400

Ile Ile Val Ser Phe Ser Ala Arg Arg Phe
 405 410

<210> 155

<211> 703

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA00803

<400> 155

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cggccgttct gttaaagatt ggtctggcca tttcctccat atg ggg gtg tcc gcg 115
 Met Gly Val Ser Ala
 1 5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
 Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
 10 15 20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
 Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
 25 30 35

gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
 Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
 40 45 50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
 Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
 55 60 65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
 Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
 70 75 80 85

gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg 403
 Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
 90 95 100

att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg 451
 Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
 105 110 115

ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg 499
 Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp

120	125	130	
att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt			547
Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser			
135	140	145	
gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc			595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu			
150	155	160	165
ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca caa cct gga			643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Gln Pro Gly			
	170	175	180
cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg			691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro			
	185	190	195
ttg ctt att aca			703
Leu Leu Ile Thr			
200			
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<213> <i>Corynebacterium glutamicum</i>			
<400> 156			
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Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val			
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Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly			
	35	40	45
Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr			
	50	55	60
Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp			
	65	70	75
Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile			
	85	90	95
Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile			
	100	105	110
Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr			
	115	120	125
Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro			
	130	135	140
Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr			

145	150	155	160
Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp			
	165	170	175
Leu Pro Gln Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr			
	180	185	190
Leu Ile Leu Phe Pro Leu Leu Ile Thr			
195	200		

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 <211> 1014
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(991)
 <223> RXA01407

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 ctggttgccc cagtgatcgc cccacttctg ggaggtcttc ttg caa gat acc att 115
 Leu Gln Asp Thr Ile
 1 5
 ggt tgc cga tgg atc ttc ctc ctc aac gtg ccc tta gga atc atc gcg 163
 Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro Leu Gly Ile Ile Ala
 10 15 20
 atc atg gct gga cta ttc atc cag ccc aag aac acg gcc gtg aat gtg 211
 Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn Thr Ala Val Asn Val
 25 30 35
 aag cga ttt gat cgg cca ggt ttc ctc ggc gca atg ctg gtg atg gtg 259
 Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala Met Leu Val Met Val
 40 45 50
 gcg caa gcc gtg att gcg gag tta att tgc agc aga agt ccg gcc gca 307
 Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser Arg Ser Pro Ala Ala
 55 60 65
 ctt act atc tgt gca tgc ctc gtc tta agt gct gcg gtg gta tgc ggt 355
 Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala Ala Val Val Cys Gly
 70 75 80 85
 ttt gta gtg cgc tgg ctg cga gtt cca ggc cga ctt ttt gat ctc agc 403
 Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg Leu Phe Asp Leu Ser
 90 95 100
 atc atg cgc atc cca ggt ttc cga gtg ggt aat tcc tcc gga agt atc 451
 Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn Ser Ser Gly Ser Ile
 105 110 115

tac cgc ttg gta atc acc gca gca cca ttc atg ttc act ttg ctc ttc 499
 Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met Phe Thr Leu Leu Phe
 120 125 130

caa gtg gcg ttt ggg tgg tct gca aca tta gcg ggt gcc atg gtg gtc 547
 Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala Gly Ala Met Val Val
 135 140 145

gca cta ttc gca ggc aac gtg gca atc aaa cct ttc acc acg ccg atc 595
 Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro Phe Thr Thr Pro Ile
 150 155 160 165

att aaa cgc tgg aat ttc aaa cca gta ctg gtc ttt tct aac gct gct 643
 Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val Phe Ser Asn Ala Ala
 170 175 180

ggc gcc ttg gta ttg gca act ttt ttg ttc gtt cgt gca gat acc cca 691
 Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val Arg Ala Asp Thr Pro
 185 190 195

ctg gtt ctc atc gtg ctg ctg ctc ttt gtt tcg ggc gca tta agg tcc 739
 Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser Gly Ala Leu Arg Ser
 200 205 210

ctc ggt ttc agc gcc tac aac acc ttg cag ttt gtc gat atc tca cca 787
 Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe Val Asp Ile Ser Pro
 215 220 225

gaa caa acc agc aac gcc aac gtg tta tca gca acc ctg cac caa cta 835
 Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala Thr Leu His Gln Leu
 230 235 240 245

ggc atg tct ttg ggt att gcg gta gca gtc atc gcc atg tcc ctt gca 883
 Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile Ala Met Ser Leu Ala
 250 255 260

ccc acc gcc aac tgg gca ttc cca ctg gca gca gcg ttg ttc ctc att 931
 Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala Ala Leu Phe Leu Ile
 265 270 275

cct cta atc ggc gca cta tct ttg cct cgc gac ggc ggt gcc cga gcc 979
 Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp Gly Gly Ala Arg Ala
 280 285 290

ttt tcc tcc tct tagaaaccca cttctgaaag gta 1014
 Phe Ser Ser Ser
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<210> 158
 <211> 297
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 158
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 20 25 30
 Thr Ala Val Asn Val Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala
 35 40 45
 Met Leu Val Met Val Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser
 50 55 60
 Arg Ser Pro Ala Ala Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala
 65 70 75 80
 Ala Val Val Cys Gly Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg
 85 90 95
 Leu Phe Asp Leu Ser Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn
 100 105 110
 Ser Ser Gly Ser Ile Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met
 115 120 125
 Phe Thr Leu Leu Phe Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala
 130 135 140
 Gly Ala Met Val Val Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro
 145 150 155 160
 Phe Thr Thr Pro Ile Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val
 165 170 175
 Phe Ser Asn Ala Ala Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val
 180 185 190
 Arg Ala Asp Thr Pro Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser
 195 200 205
 Gly Ala Leu Arg Ser Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe
 210 215 220
 Val Asp Ile Ser Pro Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala
 225 230 235 240
 Thr Leu His Gln Leu Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile
 245 250 255
 Ala Met Ser Leu Ala Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala
 260 265 270
 Ala Leu Phe Leu Ile Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp
 275 280 285
 Gly Gly Ala Arg Ala Phe Ser Ser Ser
 290 295

<210> 159

<211> 324
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(301)  
<223> RXA01408
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Met Arg Asn Asp Arg
1 5

tcc ttt agc gtt ccc att gcg cta ctt gcc gcg gga gca ctg ttt cta 163
Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala Gly Ala Leu Phe Leu
10 15 20

gaa atc ctc gac ggc acc atc ctg aca acc gca gtg cca gct att gct 211
Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala Val Pro Ala Ile Ala
25 30 35

cgt gac ttc ggt att gac gcc gtg gat gtc agc att gca ctg gtt gct 259
Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser Ile Ala Leu Val Ala
40 45 50

tac ttg gca gcc gca gca gct ggc att ccg ctg cag ggt ggc 301
Tyr Leu Ala Ala Ala Ala Ala Gly Ile Pro Leu Gln Gly Gly
55 60 65

tagcggatcg atttggtgtg cgc 324

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<210> 160
<211> 67
<212> PRT
<213> Corynebacterium glutamicum
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      20          25          30
Val Pro Ala Ile Ala Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser
      35          40          45
Ile Ala Leu Val Ala Tyr Leu Ala Ala Ala Ala Ala Gly Ile Pro Leu
      50          55          60
Gln Gly Gly
  65

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<400> 161																60
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Met Arg Ser Gly Asn																5
1																
gcc aat cgc gtc ttc ata ggt gtt acc atc ctg ctg ttt act gca gga																163
Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu Leu Phe Thr Ala Gly																20
10 15																
tgg gca gcc aat cat ttc gcg tca gtg ttg gtg ttg atc cgt gaa caa																211
Trp Ala Ala Asn His Phe Ala Ser Val Leu Val Leu Ile Arg Glu Gln																35
25 30																
tta gac gta tca agc gtg ctg gtc aac ggc gct ttt ggt att tat gca																259
Leu Asp Val, Ser Ser Val Leu Val Asn Gly Ala Phe Gly Ile Tyr Ala																50
40 45																
ctg gga ctt ctt cca agt ttg ctc gca ggc ggt gtg ctt gcc gac cgt																307
Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly Val Leu Ala Asp Arg																65
55 60																
ttt ggt gcc cgc atg gtg gta ctc acc gga ggt gta ctt tct gcg ctt																355
Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly Val Leu Ser Ala Leu																85
70 75 80																
gga aac ctt tct ctt tta gcg ttt cat gat ggt cct tcc ctc ctg gta																403
Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly Pro Ser Leu Leu Val																100
90 95																
gga cga ttc atc gtt ggt ctg ggc gtt gga tta gtc gtc agc gcg ggc																451
Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu Val Val Ser Ala Gly																115
105 110																
acc gca tgg gcg ggc aga ttg cgc gga gca agc ggc gtg aca ttg gcc																499
Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser Gly Val Thr Leu Ala																130
120 125																
ggc att att ctg acc gcc ggt ttc atg atg ggg ccg att gtg aca agt																547
Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly Pro Ile Val Thr Ser																145
135 140																
ggg ttg ggg atg gcg tcg aca agc att att acg ccc ttt gcc ata agc																595
Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr Pro Phe Ala Ile Ser																165
150 155 160																

gtt gcc ctc tcg ctg atc gcg gtg gtt gtg gga ttt gcg ctt ggc gat	643
Val Ala Leu Ser Leu Ile Ala Val Val Val Gly Phe Ala Leu Gly Asp	
170 175 180	
gcc cgc agc acc ccg agc gca ctt ggc gca tcc agc gga atc aaa cac	691
Ala Arg Ser Thr Pro S r Ala Leu Gly Ala Ser Ser Gly Ile Lys His	
185 190 195	
gaa cga agc atg aaa aag gcc ctc gcg gtg tcc ttg ccg atg gca att	739
Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser Leu Pro Met Ala Ile	
200 205 210	
tgg gtg ttc agc tgc atc acc acc tcc ctg atc gtg atg tcc gcg cgc	787
Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile Val Met Ser Ala Arg	
215 220 225	
atc gac tcc acc ttc ggc aac gcc att ctt ctc ccc gga atc ggc gcg	835
Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu Pro Gly Ile Gly Ala	
230 235 240 245	
gcg atc gcc ttc agc gca ggc ctg atc gca caa ttt tta ggt agg aaa	883
Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln Phe Leu Gly Arg Lys	
250 255 260	
ttc gcg tgg ggt cgt ggc tcc gga atc gtg ggc gcg ctg tgt gcc ctc	931
Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly Ala Leu Cys Ala Leu	
265 270 275	
gcg ggt ttt gcg ctg gca gct ttt ggt ggc gac tcc att cca gtg tgg	979
Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp Ser Ile Pro Val Trp	
280 285 290	
ctt ttc gtt atc gcc tcg atc ctg ttc ggc acc gca tat ggc ctc tgc	1027
Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr Ala Tyr Gly Leu Cys	
295 300 305	
ctg cgc gaa ggc ctc ctc agc atc gaa act tac acg cca ctc aac cga	1075
Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr Thr Pro Leu Asn Arg	
310 315 320 325	
cgt ggc acc ggc atc ggc atc tat tat gtg ttc acg tat ttg gga ttc	1123
Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe Thr Tyr Leu Gly Phe	
330 335 340	
ggg ctg cca gtg ctt ctc gac gcc ctc ctc ccg cac ctt ggc gcc tcc	1171
Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro His Leu Gly Ala Ser	
345 350 355	
att ccg ctg tac gcg ctg gcg gcg ctc gcc ctt ggc tcc gca gta atc	1219
Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu Gly Ser Ala Val Ile	
360 365 370	
cgc ggc gta caa atc aag cgc ggg tat gtg gtt tagatttcta cctacgacct	1272
Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val	
375 380	
gaa	1275

<210> 162

<211> 384

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

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Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu Val
      20           25           30

Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala
      35           40           45

Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly
      50           55           60

Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly
      65           70           75           80

Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly
      85           90           95

Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu
      100           105           110

Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser
      115           120           125

Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly
      130           135           140

Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr
      145           150           155           160

Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val Gly
      165           170           175

Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser
      180           185           190

Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser
      195           200           205

Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile
      210           215           220

Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu
      225           230           235           240

Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln
      245           250           255

Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly

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<400> 163																
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Leu	Leu	Phe	Thr	Ala	Gly	Trp	Ala	Ala	Asn	His	Phe	Ala	Ser	Val	Leu	
1				5					10					15		
gtg	ttg	atc	cgt	gaa	caa	tta	gac	gta	tca	agc	gtg	ctg	gtc	aac	ggc	96
Val	Leu	Ile	Arg	Glu	Gln	Leu	Asp	Val	Ser	Ser	Val	Leu	Val	Asn	Gly	
			20					25					30			
gct	ttt	ggt	att	tat	gca	ctg	gga	ctt	ctt	cca	agt	ttg	ctc	gca	ggc	144
Ala	Phe	Gly	Ile	Tyr	Ala	Leu	Gly	Leu	Leu	Pro	Ser	Leu	Leu	Ala	Gly	
		35					40					45				
ggt	gtg	ctt	gcc	gac	cgt	ttt	ggt	gcc	cgc	atg	gtg	gta	ctc	acc	gga	192
Gly	Val	Leu	Ala	Asp	Arg	Phe	Gly	Ala	Arg	Met	Val	Val	Leu	Thr	Gly	
	50					55					60					
ggt	gta	ctt	tct	gcg	ctt	gga	aac	ctt	tct	ctt	tta	gcg	ttt	cat	gat	240
Gly	Val	Leu	Ser	Ala	Leu	Gly	Asn	Leu	Ser	Leu	Leu	Ala	Phe	His	Asp	
65					70				75						80	

ggt cct tcc ctc ctg gta gga cga ttc atc gtt ggt ctg ggc gtt gga	288
Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly	
85 90 95	
tta gtc gtc agc gcg ggc acc gca tgg gcg ggc aga ttg cgc gga gca	336
Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala	
100 105 110	
agc ggc gtg aca ttg gcc ggc att att ctg acc gcc ggt ttc atg atg	384
Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met	
115 120 125	
ggg ccg att gtg aca agt ggg ttg ggg atg gcg tcg aca agc att att	432
Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile	
130 135 140	
acg ccc ttt gcc ata agc gtt gcc ctc tcg ctg atc gcg gtg gtt gtg	480
Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val	
145 150 155 160	
gga ttt gcg ctt ggc gat gcc cgc agc acc ccg agc gca ctt ggc gca	528
Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala	
165 170 175	
tcc agc gga atc aaa cac gaa cga agc atg aaa aag gcc ctc gcg gtg	576
Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val	
180 185 190	
tcc ttg ccg atg gca att tgg gtg ttc agc tgc atc acc acc tcc ctg	624
Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu	
195 200 205	
atc gtg atg tcc gcg cgc atc gac tcc acc ttc ggc aac gcc att ctt	672
Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu	
210 215 220	
ctc ccc gga atc ggc gcg gcg atc gcc ttc agc gca ggc ctg atc gca	720
Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala	
225 230 235 240	
caa ttt tta ggt agg aaa ttc gcg tgg ggt cgt ggc tcc gga atc gtg	768
Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val	
245 250 255	
ggc gcg ctg tgt gcc ctc gcg ggt ttt gcg ctg gca gct ttt ggt ggc	816
Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly	
260 265 270	
gac tcc att cca gtg tgg ctt ttc gtt atc gcc tcg atc ctg ttc ggc	864
Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly	
275 280 285	
acc gca tat ggc ctc tgc ctg cgc gaa ggc ctc ctc agc atc gaa act	912
Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr	
290 295 300	

tac acg cca ctc aac cga cgt ggc acc ggc atc ggc atc tat tat gtg 960
 Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
 305 310 315 320
 ttc acg tat ttg gga ttc ggg ctg cca gtg ctt ctc gac gcc ctc ctc 1008
 Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
 325 330 335
 ccg cac ctt ggc gcc tcc att ccg ctg tac gcg ctg gcg gcg ctc gcc 1056
 Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
 340 345 350
 ctt ggc tcc gca gta atc cgc ggc gta caa atc aag cgc ggg tat gtg 1104
 Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
 355 360 365
 gtt tagatttcta cctacgacct gaa 1130
 Val

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 <211> 369
 <212> PRT
 <213> Corynebacterium glutamicum

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 Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
 35 40 45
 Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
 50 55 60
 Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
 65 70 75 80
 Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
 85 90 95
 Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
 100 105 110
 Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
 115 120 125
 Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
 130 135 140
 Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
 145 150 155 160

Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala
 165 170 175
 Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
 180 185 190
 Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
 195 200 205
 Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
 210 215 220
 Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
 225 230 235 240
 Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
 245 250 255
 Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
 260 265 270
 Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
 275 280 285
 Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
 290 295 300
 Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
 305 310 315 320
 Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
 325 330 335
 Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
 340 345 350
 Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
 355 360 365

Val

<210> 165

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> RXA02060

<400> 165

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 Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
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gca gat acc ggc cac ttg gct gag ctt cgt gaa cca ctg ggc atc att 96
 Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
 20 25 30

gat gtg gag gcc ggc aaa gtt gat cgc atg atc gaa caa gcg gca ggc 144
 Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
 35 40 45

cac ctc aag cca gtt ggc gaa aga gac ttg gtg gaa ttt gaa atg ctg 192
 His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
 50 55 60

ctg gat caa aaa tcc att gca tct cag atc ggt atg agc cct tct gca 240
 Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
 65 70 75 80

cgc cac att aag cct gag gct ttg gcg gaa cgc atc gcc gct cta cca 288
 Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
 85 90 95

gaa caa atg aag gtt aca gcc cgg gcc aag atc acc agg ctg gaa cgc 336
 Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
 100 105 110

atc taactcttat ctcaactgggc ctt 362
 Ile

<210> 166

<211> 113

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 166

Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
 1 5 10 15

Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
 20 25 30

Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
 35 40 45

His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
 50 55 60

Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
 65 70 75 80

Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
 85 90 95

Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
 100 105 110

Ile

<210> 167

<211> 1395

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1372)

<223> RXN01936

<400> 167

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                                   Val Ser Phe Arg Asp
                                   1 5

att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc 163
Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu
                                   10 15 20

tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt 211
Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val
                                   25 30 35

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg 259
Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val
                                   40 45 50

ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt 307
Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu
                                   55 60 65

tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc 355
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile
                                   70 75 80 85

tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg 403
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu
                                   90 95 100

acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct 451
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser
                                   105 110 115

tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc 499
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile
                                   120 125 130

ctt cga agt att ttg ccg att gat caa tta gcg tcg gca aca tca ctg 547
Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala Ser Ala Thr Ser Leu
                                   135 140 145

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aat atg ctg ctc atg cag acc ggc gca atc gtt ggc ccg ctg atc gca	595
Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala	
150 155 160 165	
ggg gcg ttg att ccg ctg atc ggt ttc ggg tgg ctg tat ttc ctt gat	643
Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp	
170 175 180	
gtt gtc tcc atc atc ccc aca ctg tgg gct gta tgg tca ctg cct tcg	691
Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser	
185 190 195	
atc aag cca tcc ggc aag gtg atg aag gct ggt ttc gcc agt gtg gtg	739
Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val	
200 205 210	
gat ggc ctg aag tat ttg gct ggc caa ccc gtg ttg ttg atg gtg atg	787
Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met	
215 220 225	
gtg ctg gat ctt atc gcc atg att ttc ggc atg cca cgt gcg ctt tac	835
Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr	
230 235 240 245	
ccc gag atc gca gaa gtg aac ttc ggt ggg ggt gac gcc ggt gca acg	883
Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr	
250 255 260	
atg ctg gcg ttc atg tac tca tcc atg gct gtt ggc gca gtt ctt ggc	931
Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly	
265 270 275	
ggc gtg ctg tct ggt tgg gtg gcc cgg att agc cgc cag ggt gtt gca	979
Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala	
280 285 290	
gtt tat tgg tgc atc atc gcc tgg ggc gca gcc gtt gct ttg ggt ggt	1027
Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly	
295 300 305	
gtg gca att gtt gtc agc ccc ggc gcg gtg act gcg tgg gcg tgg atg	1075
Val Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met	
310 315 320 325	
ttc atc atc atg atg gtc att ggt ggc atg gct gac atg ttc agc tcg	1123
Phe Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser	
330 335 340	
gca gtt cga aac gct att ttg cag cag tct gct gcg gaa cat gtg cag	1171
Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln	
345 350 355	
ggc cga atc caa ggt gtg tgg atc atc gtc gtg gtg ggt gga cct cgt	1219
Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg	
360 365 370	
tta gct gac gtc ctt cac ggt tgg gcc gct gag ccc ctc ggc gca ggt	1267

Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly
 375 380 385

tgg acg gta tta tgg ggc gga gta gcg gtg gtt gta ctc act gca att 1315
 Trp Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile
 390 395 400 405

tgt atg gtg gcg gtg cct aaa ttc tgg aaa tac gag aaa cca aaa att 1363
 Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile
 410 415 420

acc ggc atc taaataactta tccatgccca ttt 1395
 Thr Gly Ile

<210> 168

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
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 20 25 30

Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
 35 40 45

Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
 50 55 60

Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65 70 75 80

Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
 85 90 95

Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
 100 105 110

Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
 115 120 125

Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala
 130 135 140

Ser Ala Thr Ser Leu Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val
 145 150 155 160

Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp
 165 170 175

Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val
 180 185 190

Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly
 195 200 205
 Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val
 210 215 220
 Leu Leu Met Val Met Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met
 225 230 235 240
 Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly
 245 250 255
 Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val
 260 265 270
 Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser
 275 280 285
 Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala
 290 295 300
 Val Ala Leu Gly Gly Val Ala Ile Val Val Ser Pro Gly Ala Val Thr
 305 310 315 320
 Ala Trp Ala Trp Met Phe Ile Ile Met Met Val Ile Gly Gly Met Ala
 325 330 335
 Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala
 340 345 350
 Ala Glu His Val Gln Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val
 355 360 365
 Val Gly Gly Pro Arg Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu
 370 375 380
 Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly Gly Val Ala Val Val
 385 390 395 400
 Val Leu Thr Ala Ile Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr
 405 410 415
 Glu Lys Pro Lys Ile Thr Gly Ile
 420

<210> 169

<211> 945

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(922)

<223> FRXA01936

<400> 169

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tttgccgatt gatcaataag cgctcggaac atcactgaat atg ctg ctc atg cag 115
 Met Leu Leu Met Gln
 1 5

acc ggc gca atc gtt ggc ccg ctg atc gca ggt gcg ttg att ccg ctg 163
 Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu
 10 15 20

atc ggt ttc ggg tgg ctg tat ttc ctt gat gtt gtc tcc atc atc ccc 211
 Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro
 25 30 35

aca ctg tgg gct gta tgg tca ctg cct tcg atc aag cca tcc ggc aag 259
 Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys
 40 45 50

gtg atg aag gct ggt ttc gcc agt gtg gtg gat ggc ctg aag tat ttg 307
 Val Met Lys Ala Gly Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu
 55 60 65

gct ggc caa ccc gtg ttg ttg atg gtg atg gtg ctg gat ctt atc gcc 355
 Ala Gly Gln Pro Val Leu Leu Met Val Met Val Leu Asp Leu Ile Ala
 70 75 80 85

atg att ttc ggc atg cca cgt gcg ctt tac ccc gag atc gca gaa gtg 403
 Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val
 90 95 100

aac ttc ggt ggg ggt gac gcc ggt gca acg atg ctg gcg ttc atg tac 451
 Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr
 105 110 115

tca tcc atg gct gtt ggc gca gtt ctt ggc ggc gtg ctg tct ggt tgg 499
 Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp
 120 125 130

gtg gcc cgg att agc cgc cag ggt gtt gca gtt tat tgg tgc atc atc 547
 Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile
 135 140 145

gcc tgg ggc gca gcc gtt gct ttg ggt ggt gtg gca att gtt gtc agc 595
 Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val Ala Ile Val Val Ser
 150 155 160 165

ccc ggc gcg gtg act gcg tgg gcg tgg atg ttc atc atc atg atg gtc 643
 Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe Ile Ile Met Met Val
 170 175 180

att ggt ggc atg gct gac atg ttc agc tcg gca gtt cga aac gct att 691
 Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile
 185 190 195

ttg cag cag tct gct gcg gaa cat gtg cag ggc cga atc caa ggt gtg 739
 Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly Arg Ile Gln Gly Val

200	205	210	
tgg atc atc gtc gtg gtg ggt gga cct cgt tta gct gac gtc ctt cac			787
Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu Ala Asp Val Leu His			
215	220	225	
ggt tgg gcc gct gag ccc ctc ggc gca ggt tgg acg gta tta tgg ggc			835
Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly			
230	235	240	245
gga gta gcg gtg gtt gta ctc act gca att tgt atg gtg gcg gtg cct			883
Gly Val Ala Val Val Val Leu Thr Ala Ile Cys Met Val Ala Val Pro			
250	255	260	
aaa ttc tgg aaa tac gag aaa cca aaa att acc ggc atc taaataactta			932
Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr Gly Ile			
265	270		
tccatgccca ttt			945
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<400> 170			
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20	25	30	
Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile			
35	40	45	
Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val Asp			
50	55	60	
Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met Val			
65	70	75	80
Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro			
85	90	95	
Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met			
100	105	110	
Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly			
115	120	125	
Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val			
130	135	140	
Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val			
145	150	155	160

Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe
 165 170 175

Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala
 180 185 190

Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly
 195 200 205

Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu
 210 215 220

Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp
 225 230 235 240

Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile Cys
 245 250 255

Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr
 260 265 270

Gly Ile

<210> 171
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(526)
 <223> FRXA01937

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 Val Ser Phe Arg Asp
 1 5

att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc 163
 Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu
 10 15 20

tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt 211
 Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val
 25 30 35

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg 259
 Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val
 40 45 50

ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt 307
 Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu
 55 60 65

tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc 355
 Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile
 70 75 80 85

tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg 403
 Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu
 90 95 100

acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct 451
 Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser
 105 110 115

tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc 499
 Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile
 120 125 130

ctt cga agt att ttg ccg att gat caa taagcgctcgg caacatcact 546
 Leu Arg Ser Ile Leu Pro Ile Asp Gln
 135 140

gaa 549

<210> 172

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
 1 5 10 15

Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
 20 25 30

Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
 35 40 45

Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
 50 55 60

Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65 70 75 80

Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
 85 90 95

Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
 100 105 110

Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
 115 120 125

Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln
 130 135 140

<210> 173
 <211> 1242
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1219)
 <223> RXN01010

<400> 173

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aaaagatctg gcaggggggtt taggcataga ttaggaactt atg aag aaa ctg caa 115
                                         Met Lys Lys Leu Gln
                                         1 5

atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163
Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln
                        10 15 20

gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211
Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser
                        25 30 35

gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259
Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala
                        40 45 50

acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307
Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His
                        55 60 65

aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355
Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu
                        70 75 80 85

ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr
                        90 95 100

att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451
Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
                        105 110 115

cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
                        120 125 130

gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly
                        135 140 145

gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595
Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala
                        150 155 160 165

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gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643
 Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
 170 175 180

tca gca tcg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc 691
 Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
 185 190 195

atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc 739
 Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
 200 205 210

att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt gat 787
 Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asp
 215 220 225

gct gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc ctg gct gcg ttc 835
 Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Leu Ala Ala Phe
 230 235 240 245

ttt gcc tcc cgc aag att ggc gat ttg gca gac aaa ttt ggt gtg cgc 883
 Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys Phe Gly Val Arg
 250 255 260

gcg gtg ctc att gtc agt gct gtc atc ggt acc atc gca ctc gca ctg 931
 Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr Ile Ala Leu Ala Leu
 265 270 275

ctg ccg atc gca ccg tgg atc att gtg gtg gcc gta ctg tgg gcc ttc 979
 Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala Val Leu Trp Ala Phe
 280 285 290

gca gta gca gca gca caa gga atc caa gca acc gtc aac ttg gct gtc 1027
 Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr Val Asn Leu Ala Val
 295 300 305

atc gga agc ccc ggt gga tca tcg ctg ctt tct acc gtg cag gct ttc 1075
 Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser Thr Val Gln Ala Phe
 310 315 320 325

cga ttc ttc gga tca gcg gca gca cca gtg aca ttc ctt cct atc tat 1123
 Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr Phe Leu Pro Ile Tyr
 330 335 340

atg ggc atc ggc tcg ggg gcg ttt tgg gtc agc gcg gta gcg ctg ttc 1171
 Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser Ala Val Ala Leu Phe
 345 350 355

ttc gtt gcc atc gcc cag tgg ctc aac ccg cag cgg gtg gag cgg ggc 1219
 Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln Arg Val Glu Arg Gly
 360 365 370

tgagggagac gtcgagaagc gtc 1242

<210> 174

<211> 373

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 174

Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
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Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
 20 25 30

Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
 35 40 45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
 50 55 60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
 65 70 75 80

Pro Leu Ala Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
 85 90 95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
 100 105 110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
 115 120 125

Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
 130 135 140

Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
 145 150 155 160

Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
 165 170 175

Val Val Pro Pro Pro Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val
 180 185 190

Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
 195 200 205

Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
 210 215 220

Gln Phe Gly Leu Asp Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly
 225 230 235 240

Gly Leu Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
 245 250 255

Lys Phe Gly Val Arg Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr
 260 265 270

Ile Ala Leu Ala Leu Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala

275	280	285
Val Leu Trp Ala Phe Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr 290	295	300
Val Asn Leu Ala Val Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser 305	310	315 320
Thr Val Gln Ala Phe Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr 325	330	335
Phe Leu Pro Ile Tyr Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser 340	345	350
Ala Val Ala Leu Phe Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln 355	360	365
Arg Val Glu Arg Gly 370		
<210> 175		
<211> 871		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(871)		
<223> FRXA01010		
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aaaagatctg gcaggggggt taggcataga ttaggaactt atg aag aaa ctg caa 115		
		Met Lys Lys Leu Gln 5
atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163		
Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln	10	15 20
gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211		
Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser	25	30 35
gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259		
Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala	40	45 50
acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307		
Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His	55	60 65
aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355		
Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu	70	75 80 85

ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
 Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr
 90 95 100

att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451
 Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
 105 110 115

cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
 Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
 120 125 130

gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
 Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly
 135 140 145

gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595
 Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala
 150 155 160 165

gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643
 Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
 170 175 180

tca gca ttg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc 691
 Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
 185 190 195

atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc 739
 Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
 200 205 210

att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt aat 787
 Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asn
 215 220 225

act gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc cgg gct gcg ttc 835
 Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Arg Ala Ala Phe
 230 235 240 245

ttt gcc tcc cgc aag ata ggc gat ttg gca gac aaa 871
 Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys
 250 255

<210> 176

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
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Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
 20 25 30

Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
 35 40 45
 Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
 50 55 60
 Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
 65 70 75 80
 Pro Leu Ala Leu Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
 85 90 95
 Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
 100 105 110
 Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
 115 120 125
 Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
 130 135 140
 Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
 145 150 155 160
 Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
 165 170 175
 Val Val Pro Pro Pro Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val
 180 185 190
 Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
 195 200 205
 Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
 210 215 220
 Gln Phe Gly Leu Asn Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly
 225 230 235 240
 Gly Arg Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
 245 250 255

Lys

<210> 177
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> RXN03142

<400> 177
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aaaaccacac ccacgcgaac caacggcact gttcactcca gtg ttt att ttg ggc 115
Val Phe Ile Leu Gly
1 5

tgg ctc gtc aac ttg acc cag tac ttg agc ttc tac ttc ctg atc aca 163
Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe Tyr Phe Leu Ile Thr
10 15 20

gtc atg gcg ctg tat gcg atg gaa agc ttc gcc gtt tca gag gcc gct 211
Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala Val Ser Glu Ala Ala
25 30 35

gtc gga ttt gcg gcc agc tcc ttt gtt atc ggc gca acc gtg gct cgt 259
Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly Ala Thr Val Ala Arg
40 45 50

gtg ttc gcg gga tgg acg tcc gac cgt ttt ggt aaa aaa cag atc ctg 307
Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly Lys Lys Gln Ile Leu
55 60 65

ctc atc ttt gtc ggc ttg gaa gcg gta gca tca cta ttc tat att cca 355
Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser Leu Phe Tyr Ile Pro
70 75 80 85

gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt ttt 403
Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly Phe
90 95 100

tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc gtg 451
Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser Val
105 110 115

att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc gga 499
Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu Gly
120 125 130

tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt atc 547
Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val Ile
135 140 145

gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc agt 595
Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr Ser
150 155 160 165

gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc att 643
Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe Ile
170 175 180

aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag act 691
Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys Thr
185 190 195

gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct gtc 739
Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala Val

200	205	210	
gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg caa Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala Gln 215 220 225			787
gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat gcg Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala 230 235 240 245			835
gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac aaa Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp Lys 250 255 260			883
cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc ctc His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala Leu 265 270 275			931
gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt ctc Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val Leu 280 285 290			979
gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc gca Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala Ala 295 300 305			1027
caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc ggt Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser Gly 310 315 320 325			1075
att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc cca Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly Pro 330 335 340			1123
atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg tac Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met Tyr 345 350 355			1171
gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg gtt Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu Val 360 365 370			1219
gct ttg ggt agg aaa gct agc cac taagtttagag cattttattg agc Ala Leu Gly Arg Lys Ala Ser His 375 380			1266

<210> 178

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Val	Phe	Ile	Leu	Gly	Trp	Leu	Val	Asn	Leu	Thr	Gln	Tyr	Leu	Ser	Phe
1				5					10					15	

Tyr	Phe	Leu	Ile	Thr	Val	Met	Ala	Leu	Tyr	Ala	Met	Glu	Ser	Phe	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Val	Ser	Glu	Ala	Ala	Val	Gly	Phe	Ala	Ala	Ser	Ser	Phe	Val	Ile	Gly
35					40					45					
Ala	Thr	Val	Ala	Arg	Val	Phe	Ala	Gly	Trp	Thr	Ser	Asp	Arg	Phe	Gly
50					55					60					
Lys	Lys	Gln	Ile	Leu	Leu	Ile	Phe	Val	Gly	Leu	Glu	Ala	Val	Ala	Ser
65					70					75					
Leu	Phe	Tyr	Ile	Pro	Ala	Ala	Ser	Leu	Pro	Ala	Leu	Val	Ala	Val	Arg
85					90					95					
Phe	Val	His	Gly	Phe	Ser	Tyr	Ser	Leu	Ala	Ser	Thr	Ala	Val	Met	Ala
100					105					110					
Leu	Val	Gln	Ser	Val	Ile	Pro	Ala	Ser	Arg	Arg	Ala	Glu	Gly	Thr	Gly
115					120					125					
Tyr	Phe	Ala	Leu	Gly	Ser	Thr	Leu	Ala	Thr	Ala	Phe	Gly	Pro	Ala	Ile
130					135					140					
Ala	Leu	Phe	Val	Ile	Asp	Asp	Phe	Asn	Tyr	Asn	Thr	Leu	Phe	Trp	Ile
145					150					155					
Thr	Thr	Ala	Thr	Ser	Val	Phe	Gly	Leu	Ile	Leu	Thr	Val	Leu	Ile	Arg
165					170					175					
Lys	Pro	Glu	Phe	Ile	Lys	Asn	Ala	Glu	His	Gly	Arg	Val	Lys	Pro	Val
180					185					190					
Trp	Ser	Ile	Lys	Thr	Val	Val	His	Pro	Ser	Val	Met	Leu	Ile	Gly	Phe
195					200					205					
Phe	Met	Leu	Ala	Val	Gly	Leu	Ala	Tyr	Ala	Gly	Val	Ile	Thr	Phe	Leu
210					215					220					
Asn	Gly	Phe	Ala	Gln	Asp	Thr	Gly	Leu	Thr	Ala	Gly	Ala	Gly	Leu	Phe
225					230					235					
Phe	Ile	Ala	Tyr	Ala	Val	Ala	Met	Leu	Val	Met	Arg	Phe	Phe	Leu	Gly
245					250					255					
Arg	Ile	Gln	Asp	Lys	His	Gly	Asp	Asn	Pro	Val	Ile	Tyr	Phe	Gly	Leu
260					265					270					
Ile	Ser	Phe	Ala	Leu	Ala	Leu	Gly	Leu	Met	Ala	Leu	Ala	Thr	Glu	Asp
275					280					285					
Trp	His	Ile	Val	Leu	Ala	Gly	Ala	Leu	Thr	Gly	Leu	Gly	Tyr	Gly	Thr
290					295					300					
Ile	Met	Pro	Ala	Ala	Gln	Ala	Ile	Ala	Val	Asp	Ser	Val	Pro	Ser	Thr
305					310					315					
Gln	Val	Gly	Ser	Gly	Ile	Ser	Thr	Leu	Phe	Leu	Phe	Thr	Asp	Ile	Gly

	325		330		335
Ile Gly Leu Gly Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly					
	340		345		350
Tyr Asn Val Met Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly					
	355		360		365
Val Leu Tyr Leu Val Ala Leu Gly Arg Lys Ala Ser His					
	370		375		380

<210> 179

<211> 914

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(891)

<223> FRXA01150

<400> 179

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1 5 10 15	
ttt tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc	96
Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser	
20 25 30	
gtg att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc	144
Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu	
35 40 45	
gga tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt	192
Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val	
50 55 60	
atc gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc	240
Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr	
65 70 75 80	
agt gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc	288
Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe	
85 90 95	
att aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag	336
Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys	
100 105 110	
act gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct	384
Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala	
115 120 125	
gtc gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg	432
Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala	

130	135	140	
caa gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat			480
Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr			
145	150	155	160
gcg gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac			528
Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp			
	165	170	175
aaa cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc			576
Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala			
	180	185	190
ctc gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt			624
Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val			
	195	200	205
ctc gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc			672
Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala			
	210	215	220
gca caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc			720
Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser			
	225	230	240
ggt att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc			768
Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly			
	245	250	255
cca atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg			816
Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met			
	260	265	270
tac gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg			864
Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu			
	275	280	285
ggt gct ttg ggt agg aaa gct agc cac taagtttagag cattttattg			911
Val Ala Leu Gly Arg Lys Ala Ser His			
	290	295	
agc			914

<210> 180

<211> 297

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly
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Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser
 20 25 30

Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu
 35 40 45
 Gly Ser Thr Leu Ala Thr Ala Ph Gly Pro Ala Ile Ala Leu Phe Val
 50 55 60
 Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
 65 70 75 80
 Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
 85 90 95
 Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
 100 105 110
 Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
 115 120 125
 Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala
 130 135 140
 Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr
 145 150 155 160
 Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp
 165 170 175
 Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala
 180 185 190
 Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val
 195 200 205
 Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala
 210 215 220
 Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser
 225 230 235 240
 Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly
 245 250 255
 Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met
 260 265 270
 Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu
 275 280 285
 Val Ala Leu Gly Arg Lys Ala Ser His
 290 295

<210> 181

<211> 1341

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1318)

<223> RXN02964

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aaaattgcat gatgcaataa tttcgattta aaggagaaca gtg tcc gta gct gaa 115
 Val Ser Val Ala Glu
 1 5

gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
 Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
 10 15 20

ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
 Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
 25 30 35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259
 Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
 40 45 50

tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc 307
 Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
 55 60 65

tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc 355
 Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
 70 75 80 85

cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg 403
 Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
 90 95 100

cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt 451
 Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
 105 110 115

gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca 499
 Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
 120 125 130

cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct 547
 Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
 135 140 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat 595
 Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp
 150 155 160 165

tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg 643
 Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu
 170 175 180

atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct 691

Ile	Ala	Val	Val	Phe	Met	Tyr	Phe	Lys	Thr	Ser	Asp	Pro	Glu	Pro	Ser		
			185					190					195				
ggg	gaa	cca	gcc	aag	ttc	agc	ttc	aaa	tct	att	atg	aac	cca	aag	atc	739	
Gly	Glu	Pro	Ala	Lys	Phe	Ser	Phe	Lys	Ser	Ile	Met	Asn	Pro	Lys	Ile		
		200					205					210					
atc	ccc	atc	ggc	atc	ttt	atc	ttg	ctt	att	tgc	ttt	gct	tac	tct	ggc	787	
Ile	Pro	Ile	Gly	Ile	Phe	Ile	Leu	Leu	Ile	Cys	Phe	Ala	Tyr	Ser	Gly		
	215					220				225							
gtc	att	gcc	tac	atc	aac	gca	ttt	gct	gaa	gaa	cgc	gat	ctg	att	acg	835	
Val	Ile	Ala	Tyr	Ile	Asn	Ala	Phe	Ala	Glu	Glu	Arg	Asp	Leu	Ile	Thr		
230					235				240						245		
ggg	gct	gga	ttg	ttc	ttc	att	gcc	tac	gca	gta	tca	atg	ttt	gtg	atg	883	
Gly	Ala	Gly	Leu	Phe	Phe	Ile	Ala	Tyr	Ala	Val	Ser	Met	Phe	Val	Met		
			250						255					260			
cgc	agc	ttc	ctt	ggc	aaa	ctg	cag	gac	cgt	cgc	gga	gac	aac	gtc	gtt	931	
Arg	Ser	Phe	Leu	Gly	Lys	Leu	Gln	Asp	Arg	Arg	Gly	Asp	Asn	Val	Val		
		265						270					275				
att	tac	ttt	gga	ttg	ttc	ttc	ttc	gtt	att	tcc	ttg	acg	att	ttg	tcc	979	
Ile	Tyr	Phe	Gly	Leu	Phe	Phe	Phe	Val	Ile	Ser	Leu	Thr	Ile	Leu	Ser		
	280					285					290						
ttt	gcc	act	tcc	aac	tgg	cac	gtt	gtg	ttg	tcc	gga	gtc	att	gca	ggt	1027	
Phe	Ala	Thr	Ser	Asn	Trp	His	Val	Val	Leu	Ser	Gly	Val	Ile	Ala	Gly		
	295				300						305						
ctg	gga	tac	ggc	act	ttg	atg	cca	gca	gtg	cag	tcc	atc	gct	gtt	ggt	1075	
Leu	Gly	Tyr	Gly	Thr	Leu	Met	Pro	Ala	Val	Gln	Ser	Ile	Ala	Val	Gly		
310					315					320					325		
gta	gta	gac	aaa	acc	gaa	ttc	ggg	acg	gcc	ttc	tcc	act	ttg	ttc	ctg	1123	
Val	Val	Asp	Lys	Thr	Glu	Phe	Gly	Thr	Ala	Phe	Ser	Thr	Leu	Phe	Leu		
			330						335					340			
ttt	gtg	gac	tta	ggg	ttt	ggc	ttt	gga	cct	att	atc	ctg	gga	gca	gtt	1171	
Phe	Val	Asp	Leu	Gly	Phe	Gly	Phe	Gly	Pro	Ile	Ile	Leu	Gly	Ala	Val		
		345						350					355				
tct	gcg	gca	att	ggg	ttc	gga	cct	atg	tat	gca	gca	ctg	gca	ggg	gtg	1219	
Ser	Ala	Ala	Ile	Gly	Phe	Gly	Pro	Met	Tyr	Ala	Ala	Leu	Ala	Gly	Val		
	360					365						370					
ggg	gtg	att	gcc	gga	atc	ttc	tac	ctg	ttc	aca	cac	gct	cgc	acc	gat	1267	
Gly	Val	Ile	Ala	Gly	Ile	Phe	Tyr	Leu	Phe	Thr	His	Ala	Arg	Thr	Asp		
	375					380					385						
cga	gct	aag	aat	ggc	ttt	gtt	aaa	cac	cca	gag	cct	gtc	gct	tta	gtt	1315	
Arg	Ala	Lys	Asn	Gly	Phe	Val	Lys	His	Pro	Glu	Pro	Val	Ala	Leu	Val		
390				395					400					405			
agc	tagttctttc	agctttccct	ccc													1341	
Ser																	

<210> 182

<211> 406

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Val	Ser	Val	Ala	Glu	Glu	Gly	Lys	Leu	Phe	Thr	Pro	Thr	Phe	Val	Met
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Gly	Trp	Phe	Ala	Asn	Leu	Phe	Gln	Phe	Leu	Val	Phe	Tyr	Phe	Leu	Ile
			20					25					30		
Thr	Thr	Met	Ala	Leu	Tyr	Ala	Ile	Lys	Glu	Phe	Gln	Ala	Ser	Glu	Val
		35					40					45			
Glu	Ala	Gly	Phe	Ala	Ser	Ser	Ser	Ile	Val	Ile	Gly	Ala	Val	Phe	Ser
	50					55					60				
Arg	Phe	Phe	Ser	Gly	Tyr	Ile	Ile	Asp	Arg	Phe	Gly	Arg	Arg	Lys	Ile
65					70				75						80
Val	Leu	Ile	Ser	Val	Leu	Val	Thr	Thr	Ile	Ala	Cys	Ala	Leu	Tyr	Leu
			85						90					95	
Pro	Ile	Glu	Ser	Leu	Pro	Leu	Leu	Tyr	Ala	Asn	Arg	Phe	Leu	His	Gly
			100					105					110		
Val	Gly	Tyr	Ala	Phe	Ala	Ala	Thr	Ala	Ile	Met	Ala	Met	Val	Gln	Glu
		115					120					125			
Leu	Ile	Pro	Ala	Ser	Arg	Arg	Ser	Glu	Gly	Thr	Gly	Tyr	Leu	Ala	Leu
	130					135					140				
Gly	Thr	Thr	Val	Ser	Ala	Ala	Leu	Gly	Pro	Ala	Leu	Ala	Leu	Phe	Val
145					150					155					160
Leu	Gly	Thr	Phe	Asp	Tyr	Asp	Met	Leu	Phe	Ile	Val	Val	Leu	Ala	Thr
			165						170					175	
Ser	Val	Ile	Ser	Leu	Ile	Ala	Val	Val	Phe	Met	Tyr	Phe	Lys	Thr	Ser
			180					185					190		
Asp	Pro	Glu	Pro	Ser	Gly	Glu	Pro	Ala	Lys	Phe	Ser	Phe	Lys	Ser	Ile
		195					200					205			
Met	Asn	Pro	Lys	Ile	Ile	Pro	Ile	Gly	Ile	Phe	Ile	Leu	Leu	Ile	Cys
	210					215					220				
Phe	Ala	Tyr	Ser	Gly	Val	Ile	Ala	Tyr	Ile	Asn	Ala	Phe	Ala	Glu	Glu
225					230					235					240
Arg	Asp	Leu	Ile	Thr	Gly	Ala	Gly	Leu	Phe	Phe	Ile	Ala	Tyr	Ala	Val
				245					250					255	

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
 260 265 270
 Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
 275 280 285
 Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val Leu Ser
 290 295 300
 Gly Val Ile Ala Gly Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln
 305 310 315 320
 Ser Ile Ala Val Gly Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe
 325 330 335
 Ser Thr Leu Phe Leu Phe Val Asp Leu Gly Phe Gly Phe Gly Pro Ile
 340 345 350
 Ile Leu Gly Ala Val Ser Ala Ala Ile Gly Phe Gly Pro Met Tyr Ala
 355 360 365
 Ala Leu Ala Gly Val Gly Val Ile Ala Gly Ile Phe Tyr Leu Phe Thr
 370 375 380
 His Ala Arg Thr Asp Arg Ala Lys Asn Gly Phe Val Lys His Pro Glu
 385 390 395 400
 Pro Val Ala Leu Val Ser
 405

<210> 183
 <211> 1006
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1006)
 <223> FRXA02116

<400> 183
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 aaaattgcat gatgcaataa tttcgattta aaggagaaca gtg tcc gta gct gaa 115
 Val Ser Val Ala Glu
 1 5
 gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
 Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
 10 15 20
 ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
 Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
 25 30 35
 tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259

Tyr	Ala	Ile	Lys	Glu	Phe	Gln	Ala	Ser	Glu	Val	Glu	Ala	Gly	Phe	Ala		
		40					45					50					
tcc	agc	tca	att	gtt	atc	ggc	gca	gtc	ttt	tcc	agg	ttt	ttc	tcc	ggc	307	
Ser	Ser	Ser	Ile	Val	Ile	Gly	Ala	Val	Phe	Ser	Arg	Phe	Phe	Ser	Gly		
	55					60					65						
tat	att	att	gac	cgt	ttt	ggg	cga	cgc	aag	att	gtg	ctc	atc	tca	gtc	355	
Tyr	Ile	Ile	Asp	Arg	Phe	Gly	Arg	Arg	Lys	Ile	Val	Leu	Ile	Ser	Val		
	70				75					80					85		
cta	gtc	act	acc	att	gcg	tgt	gcc	ttg	tac	ctt	ccc	atc	gaa	tca	ttg	403	
Leu	Val	Thr	Thr	Ile	Ala	Cys	Ala	Leu	Tyr	Leu	Pro	Ile	Glu	Ser	Leu		
				90					95					100			
cca	ttg	cta	tac	gca	aac	agg	ttc	ctc	cac	ggg	gtt	gga	tac	gct	ttt	451	
Pro	Leu	Leu	Tyr	Ala	Asn	Arg	Phe	Leu	His	Gly	Val	Gly	Tyr	Ala	Phe		
			105					110					115				
gct	gcc	acc	gcg	atc	atg	gca	atg	gtc	cag	gag	ctc	att	cca	gcg	tca	499	
Ala	Ala	Thr	Ala	Ile	Met	Ala	Met	Val	Gln	Glu	Leu	Ile	Pro	Ala	Ser		
		120					125					130					
cga	cgt	tcc	gaa	ggg	act	ggg	tac	ctg	gca	ttg	ggc	act	acc	gtt	tct	547	
Arg	Arg	Ser	Glu	Gly	Thr	Gly	Tyr	Leu	Ala	Leu	Gly	Thr	Thr	Val	Ser		
	135					140					145						
gca	gca	ctt	gga	cca	gcc	cta	gca	ctt	ttt	gtc	cta	gga	aca	ttt	gat	595	
Ala	Ala	Leu	Gly	Pro	Ala	Leu	Ala	Leu	Phe	Val	Leu	Gly	Thr	Phe	Asp		
	150				155					160					165		
tac	gac	atg	ctg	ttt	atc	gtg	gtc	ttg	gca	acc	tcg	gtc	atc	tct	ttg	643	
Tyr	Asp	Met	Leu	Phe	Ile	Val	Val	Leu	Ala	Thr	Ser	Val	Ile	Ser	Leu		
				170					175					180			
atc	gcc	gtc	gtg	ttc	atg	tac	ttt	aag	acc	agc	gac	cct	gag	cct	tct	691	
Ile	Ala	Val	Val	Phe	Met	Tyr	Phe	Lys	Thr	Ser	Asp	Pro	Glu	Pro	Ser		
			185					190					195				
ggg	gaa	cca	gcc	aag	ttc	agc	ttc	aaa	tct	att	atg	aac	cca	aag	atc	739	
Gly	Glu	Pro	Ala	Lys	Phe	Ser	Phe	Lys	Ser	Ile	Met	Asn	Pro	Lys	Ile		
		200					205					210					
atc	ccc	atc	ggc	atc	ttt	atc	ttg	ctt	att	tgc	ttt	gct	tac	tct	ggc	787	
Ile	Pro	Ile	Gly	Ile	Phe	Ile	Leu	Leu	Ile	Cys	Phe	Ala	Tyr	Ser	Gly		
	215					220					225						
gtc	att	gcc	tac	atc	aac	gca	ttt	gct	gaa	gaa	cgc	gat	ctg	att	acg	835	
Val	Ile	Ala	Tyr	Ile	Asn	Ala	Phe	Ala	Glu	Glu	Arg	Asp	Leu	Ile	Thr		
	230				235					240					245		
ggg	gct	gga	ttg	ttc	ttc	att	gcc	tac	gca	gta	tca	atg	ttt	gtg	atg	883	
Gly	Ala	Gly	Leu	Phe	Phe	Ile	Ala	Tyr	Ala	Val	Ser	Met	Phe	Val	Met		
				250					255					260			
cgc	agc	ttc	ctt	ggc	aaa	ctg	cag	gac	cgt	cgc	gga	gac	aac	gtc	gtt	931	
Arg	Ser	Phe	Leu	Gly	Lys	Leu	Gln	Asp	Arg	Arg	Gly	Asp	Asn	Val	Val		

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Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
35 40 45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
50 55 60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
65 70 75 80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
85 90 95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
100 105 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
115 120 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
130 135 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
145 150 155 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
165 170 175

Ser, Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
180 185 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
195 200 205

Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys

210

215

220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
 225 230 235 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
 245 250 255

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
 260 265 270

Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
 275 280 285

Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val
 290 295 300

<210> 185

<211> 568

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(568)

<223> RXA00858

<400> 185

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tcttaaattg tctaaccaag aaccggaggt tctttttgtc atg gaa gta aac tta 115
 Met Glu Val Asn Leu
 1 5

gcc aca tgg cta atc act atc gca gtg att gct ggc ttc ttc att ttc 163
 Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala Gly Phe Phe Ile Phe
 10 15 20

gat ttc tat tcc cac gtc cgc acc cca cac gag ccc act atc aaa gaa 211
 Asp Phe Tyr Ser His Val Arg Thr Pro His Glu Pro Thr Ile Lys Glu
 25 30 35

tcc gca tgg tgg agc ctc ttc tac gta gcc ctc gcc tgt gtt ttc ggc 259
 Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu Ala Cys Val Phe Gly
 40 45 50

gtg ttc ctc tgg ttt gct tgg ggc gag cca ggt aac cca cac cag cac 307
 Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly Asn Pro His Gln His
 55 60 65

ggc att gag ttc ttc acc ggt tac gtg aca gag aag gcg ttg agt gtt 355
 Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu Lys Ala Leu Ser Val
 70 75 80 85

gat aac ctc ttc atc ttc gcg ctg atc atg ggt tct ttc aag att cct 403
 Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly Ser Phe Lys Ile Pro

	90	95	100	
cgc aag tac cag cag aag gtt ctg ctc atc ggt atc gcg ctg gca ctg				451
Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly Ile Ala Leu Ala Leu				
	105	110	115	
gtc ttc cgc ctg gca ttc atc ctc gca ggt gct gca gtt atc gaa gcc				499
Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala Ala Val Ile Glu Ala				
	120	125	130	
tgg tcc gat gtc ttc tac atc ttc tcc atc tgg ctg atc tac acc gct				547
Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp Leu Ile Tyr Thr Ala				
	135	140	145	
gtg aag gct cct gtg cac gag				568
Val Lys Ala Pro Val His Glu				
	150	155		

<210> 186

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Glu Val Asn Leu Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala			
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Gly Phe Phe Ile Phe Asp Phe Tyr Ser His Val Arg Thr Pro His Glu			
	20	25	30
Pro Thr Ile Lys Glu Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu			
	35	40	45
Ala Cys Val Phe Gly Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly			
	50	55	60
Asn Pro His Gln His Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu			
	65	70	75
Lys Ala Leu Ser Val Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly			
	85	90	95
Ser Phe Lys Ile Pro Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly			
	100	105	110
Ile Ala Leu Ala Leu Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala			
	115	120	125
Ala Val Ile Glu Ala Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp			
	130	135	140
Leu Ile Tyr Thr Ala Val Lys Ala Pro Val His Glu			
	145	150	155

<210> 187

<211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA02305

<400> 187

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caaacgatga cttcgatccc gaaaagtgga ggaacatgta atg cca gcc ttt gag 115
 Met Pro Ala Phe Glu
 1 5

gca atg cca gga atg ccg tat tgg atc gac ctg tcc acc tcg gac att 163
 Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu Ser Thr Ser Asp Ile
 10 15 20

gca aaa tct gca cac ttc tac gaa aac gtt ctc ggc tgg gaa att gaa 211
 Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu Gly Trp Glu Ile Glu
 25 30 35

gaa gtc aac gat ggc tac cgc atg gct cgt ctg cag gga cta ccc gtg 259
 Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu Gln Gly Leu Pro Val
 40 45 50

gca ggg ctg atc gat cag cgc ggt gaa tca agc atc ccg gat acc tgg 307
 Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser Ile Pro Asp Thr Trp
 55 60 65

att acc tac ttc ctc tcc tac gat ctg gat gcc act gca aag aag atc 355
 Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala Thr Ala Lys Lys Ile
 70 75 80 85

gca gaa ctg ggt gga cga att ctg gcc gag cca act gac gtg cac ttg 403
 Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro Thr Asp Val His Leu
 90 95 100

gga cgc atg atc cta gct gtt gat act gcc ggc gca ctg ttc ggc gtt 451
 Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly Ala Leu Phe Gly Val
 105 110 115

att gag cca ggc agc gag gaa tca ttc gtc gct gct ggt gaa cca ggc 499
 Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala Ala Gly Glu Pro Gly
 120 125 130

aca tcc gtg tgg cat gaa ctc acc act gtc tcc aaa tat tcc gaa gct 547
 Thr Ser Val Trp His Glu Leu Thr Thr Val Ser Lys Tyr Ser Glu Ala
 135 140 145

atc gat ttc tac ggt gag ctg ttc act tgg aca acc tct gaa atg gct 595
 Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr Thr Ser Glu Met Ala
 150 155 160 165

agt gct gaa gac gat agt ttc cgc tac acc acc gca ttg gct gac ggt 643

Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr Ala Leu Ala Asp Gly
 170 175 180

tcc gcc ttt gct gga att ttt gat gcc aaa ggc cac ttc cca cct cag 691
 S r Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly His Phe Pro Pro Gln
 185 190 195

gtt cca agc ttc tgg cag tcc tac ctt ggc gtg ctc aac gcc gat gat 739
 Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val Leu Asn Ala Asp Asp
 200 205 210

gct gca gcg aag gcc aag gaa ttt ggt ggc gat gtt att cgt aag cca 787
 Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp Val Ile Arg Lys Pro
 215 220 225

tgg gac tca gaa ttt ggc cgc atg gtt ctc atc tct gat tcc act ggt 835
 Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile Ser Asp Ser Thr Gly
 230 235 240 245

gcc aca att acc ttg tgt gaa gta gag gaa tac gtc gag gaa gca gca 883
 Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr Val Glu Glu Ala Ala
 250 255 260

gaa ggc gat gat ctc ttc gac atc gat ctc agt gct ttc gaa gag cag 931
 Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser Ala Phe Glu Glu Gln
 265 270 275

ttc cgc aag caa gaa gga cag taatcctaca gcgccatgga gga 975
 Phe Arg Lys Gln Glu Gly Gln
 280

<210> 188

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Pro Ala Phe Glu Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu
 1 5 10 15

Ser Thr Ser Asp Ile Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu
 20 25 30

Gly Trp Glu Ile Glu Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu
 35 40 45

Gln Gly Leu Pro Val Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser
 50 55 60

Ile Pro Asp Thr Trp Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala
 65 70 75 80

Thr Ala Lys Lys Ile Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro
 85 90 95

Thr Asp Val His Leu Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly

100	105	110
Ala Leu Phe Gly Val Il 115	Glu Pro Gly Ser Glu Glu Ser 120	Phe Val Ala 125
Ala Gly Glu Pro Gly Thr 130	Ser Val Trp His Glu 135	Leu Thr Thr Val Ser 140
Lys Tyr Ser Glu Ala Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr 145	150	155 160
Thr Ser Glu Met Ala Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr 165	170	175
Ala Leu Ala Asp Gly Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly 180	185	190
His Phe Pro Pro Gln Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val 195	200	205
Leu Asn Ala Asp Asp Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp 210	215	220
Val Ile Arg Lys Pro Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile 225	230	235 240
Ser Asp Ser Thr Gly Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr 245	250	255
Val Glu Glu Ala Ala Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser 260	265	270
Ala Phe Glu Glu Gln Phe Arg Lys Gln Glu Gly Gln 275	280	

<210> 189
 <211> 948
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(925)
 <223> RXA00084

 <400> 189
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 tcttgaaga catcgatgcc ttcctcgacg cacagcaata atg tcc aca gct ctc 115
 Met Ser Thr Ala Leu
 1 5

 ccc gat cag ctc aag tgg gaa tac agt gcc ttc ccc gtg cag atc tcg 163
 Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe Pro Val Gln Ile Ser
 10 15 20

cag aag caa cgg ctt agt ccc ggc ttc atg cgg atc acc gtc act ggt Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg Ile Thr Val Thr Gly 25 30 35	211
gac aag ctc cga ttc ttt ggc cag tgg ggt ttg gac caa cgc atc aaa Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu Asp Gln Arg Ile Lys 40 45 50	259
ctg atc att cca agc ccg gct ggg aac atc cca gat ttc gga att ctc Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro Asp Phe Gly Ile Leu 55 60 65	307
gac gaa ccc act ccc cca ccg aca acg tgg ctt cct cgt gct aag tct Asp Glu Pro Thr Pro Pro Thr Thr Trp Leu Pro Arg Ala Lys Ser 70 75 80 85	355
ttt cca gcg gac caa cga ccg atc ttg cgc acc tac acc cca tct gcg Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr Tyr Thr Pro Ser Ala 90 95 100	403
gtc cga ccc gaa cta tgc gaa gta gac att gat atc tat ctt cac aac Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp Ile Tyr Leu His Asn 105 110 115	451
cct tcg gga cca gta tcc aga tgg gca aag aac tgc agt gtt gac gat Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn Cys Ser Val Asp Asp 120 125 130	499
gaa cta atc atc acc ggc cct gac gta cgc gca gga gaa acc ggc tac Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala Gly Glu Thr Gly Tyr 135 140 145	547
gga atc acc tat cat ccg act tct gcg atc gat cgc ctc tgt ctc atc Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp Arg Leu Cys Leu Ile 150 155 160 165	595
ggc gat tgt gca tca gct ccc gcg atc gca aat atc gtc aat caa tca Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn Ile Val Asn Gln Ser 170 175 180	643
aaa gta cct act acg gtt ttc ctc cac gta gac agc cta gaa gat gat Lys Val Pro Thr Thr Val Phe Leu His Val Asp Ser Leu Glu Asp Asp 185 190 195	691
gta ttg atc gcc gat agc tcc acc aag ctc act ttc gaa gac atc gac Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr Phe Glu Asp Ile Asp 200 205 210	739
gct tac aaa gca aag gtc ttc caa tgg gct tca gcc aat gca gca gat Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser Ala Asn Ala Ala Asp 215 220 225	787
cct tca gta cac ttc tgg atc gcc ggt gaa act agc atg gtg cgc ttc Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr Ser Met Val Arg Phe 230 235 240 245	835
att cgc aaa gaa cta atc aac agc tac cga gtt gat tcc tca cga atc	883

Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val Asp Ser Ser Arg Ile
 250 255 260

act ttc ctc ggc tac tgg aaa tac ggc cga cga acc gta gac 925
 Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg Thr Val Asp
 265 270 275

tagcttttcag attcagaccc cag 948

<210> 190

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Met Ser Thr Ala Leu Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe
 1 5 10 15

Pro Val Gln Ile Ser Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg
 20 25 30

Ile Thr Val Thr Gly Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu
 35 40 45

Asp Gln Arg Ile Lys Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro
 50 55 60

Asp Phe Gly Ile Leu Asp Glu Pro Thr Pro Pro Thr Thr Trp Leu
 65 70 75 80

Pro Arg Ala Lys Ser Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr
 85 90 95

Tyr Thr Pro Ser Ala Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp
 100 105 110

Ile Tyr Leu His Asn Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn
 115 120 125

Cys Ser Val Asp Asp Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala
 130 135 140

Gly Glu Thr Gly Tyr Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp
 145 150 155 160

Arg Leu Cys Leu Ile Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn
 165 170 175

Ile Val Asn Gln Ser Lys Val Pro Thr Thr Val Phe Leu His Val Asp
 180 185 190

Ser Leu Glu Asp Asp Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr
 195 200 205

Phe Glu Asp Ile Asp Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser
 210 215 220

Ala Asn Ala Ala Asp Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr
225 230 235 240

Ser Met Val Arg Phe Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val
245 250 255

Asp Ser Ser Arg Ile Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg
260 265 270

Thr Val Asp
275

<210> 191

<211> 468

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(445)

<223> RXA00843

<400> 191

gccctgatgc gaaaccggcg ccaacaatga tgccgacgaa ggcaaagcc actcttagga 60

tttgaataat catggaacaa accttagtag gctcaacgtt atg aaa gtc acg att 115
Met Lys Val Thr Ile
1 5

ttc cat aat ccg cgt tgt tcc aca tcc aga aat acc ctc gct tac ctc 163
Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn Thr Leu Ala Tyr Leu
10 15 20

cgc gac aag gac att gag cct gaa att gtt cag tat ctc aaa gac acg 211
Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln Tyr Leu Lys Asp Thr
25 30 35

ccc acc gct tcc gag ctc aaa gaa cta ttc aat acg ctg gga att cca 259
Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn Thr Leu Gly Ile Pro
40 45 50

gtc cac gac ggc atc aga acc cgc gaa gct gag tac aca gaa ctg ggc 307
Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu Tyr Thr Glu Leu Gly
55 60 65

ctg tca cca gaa aca cct gaa act gag ctt atc gac gcc atc gtt gcc 355
Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile Asp Ala Ile Val Ala
70 75 80 85

cat ccc agg ctc ctt cag cgt ccg atc gtg gtg acg gcc aaa ggc gcg 403
His Pro Arg Leu Leu Gln Arg Pro Ile Val Val Thr Ala Lys Gly Ala
90 95 100

cgc att gcg cgc ccc aaa atc gac gtc att gac agc atc ttg 445
Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp Ser Ile Leu

105

110

115

tgacaacatt ttgtagagca acc

468

<210> 192

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Met Lys Val Thr Ile Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn
 1 5 10 15

Thr Leu Ala Tyr Leu Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln
 20 25 30

Tyr Leu Lys Asp Thr Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn
 35 40 45

Thr Leu Gly Ile Pro Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu
 50 55 60

Tyr Thr Glu Leu Gly Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile
 65 70 75 80

Asp Ala Ile Val Ala His Pro Arg Leu Leu Gln Arg Pro Ile Val Val
 85 90 95

Thr Ala Lys Gly Ala Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp
 100 105 110

Ser Ile Leu
 115

<210> 193

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> RXA01052

<400> 193

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acgaacaacg aagagcttgc ccgagagtat cttgggtcgc atg gac aca aaa tta 115
 Met Asp Thr Lys Leu
 1 5

ggc gct gaa ttg ggt act gaa ttt gat ctc att gtt gtt ggt ttc ggc 163
 Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile Val Val Gly Phe Gly
 10 15 20

aaa gca ggc aag act atc gcg atg aaa cgc tcg gca gcg ggg gat aag 211
 Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser Ala Ala Gly Asp Lys
 25 30 35

gtc gca ctg atc gag cag agt cca cag atg tat ggc ggt acc tgc atc 259
 Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr Gly Gly Thr Cys Ile
 40 45 50

aat gta ggt tgc atc ccc acg aag aag ttg ttg ttt gag act gca acg 307
 Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu Phe Glu Thr Ala Thr
 55 60 65

ggc aag gat ttc ccg gat gcg gtt gtg gcg cgt gat cag ttg att ggc 355
 Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg Asp Gln Leu Ile Gly
 70 75 80 85

aag ctg aat gcc aag aat ctt gcg atg gcc aca gac aag ggt gtc acc 403
 Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr Asp Lys Gly Val Thr
 90 95 100

cgt cat tgatggaaaa gctacgttta cag 432
 Arg His

<210> 194

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Met Asp Thr Lys Leu Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile
 1 5 10 15

Val Val Gly Phe Gly Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser
 20 25 30

Ala Ala Gly Asp Lys Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr
 35 40 45

Gly Gly Thr Cys Ile Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu
 50 55 60

Phe Glu Thr Ala Thr Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg
 65 70 75 80

Asp Gln Leu Ile Gly Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr
 85 90 95

Asp Lys Gly Val Thr Arg His
 100

<210> 195

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA01053

<400> 195

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agccacgaaa tcacaagtaa cttcaggtag tgacactctt gtg ctg tat gcg cca 115
 Val Leu Tyr Ala Pro
 1 5

acg att gtg atc aac acg ggc tcc acg ccg gtc atc ccc aat gtc cca 163
 Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val Ile Pro Asn Val Pro
 10 15 20

ggc acc gac aat ccg cat gtt ttt gat tcc act ggc att cag cac att 211
 Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr Gly Ile Gln His Ile
 25 30 35

tcg ccc ctg ccg aag cac ctc gcg atc atc ggc ggt ggc ccc atc ggt 259
 Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly Gly Gly Pro Ile Gly
 40 45 50

ttg gaa ttt gcc acg ctt ttc agt gga caa ggc tcc aaa gtc acc atc 307
 Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly Ser Lys Val Thr Ile
 55 60 65

atc gac cgt ggt gaa ttg ccg ctg aaa aat ttc gac agg gaa gta gcg 355
 Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe Asp Arg Glu Val Ala
 70 75 80 85

gag ctg gcc aaa acc gac ctg gag gcc cgc gga atc acc ttc ctc aac 403
 Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly Ile Thr Phe Leu Asn
 90 95 100

aac gct gaa ctc acc gga ttc agc ggt gac ctc acc atc gcg ctc aaa 451
 Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu Thr Ile Ala Leu Lys
 105 110 115

gac cac gac ctc ctc gcc gac gcc gca ctt ttt gca tcg gcc gac gcc 499
 Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe Ala Ser Ala Asp Ala
 120 125 130

cgg cac cga cgg gct cgg cct tgaacaggcg ggcattcaaaa cag 543
 Arg His Arg Arg Ala Arg Pro
 135 140

<210> 196

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Val Leu Tyr Ala Pro Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val

1	5	10	15
Ile Pro Asn Val	Pro Gly Thr Asp Asn	Pro His Val Phe	Asp Ser Thr
20	25	30	
Gly Ile Gln His	Ile Ser Pro Leu	Pro Lys His Leu	Ala Ile Ile Gly
35	40	45	
Gly Gly Pro Ile	Gly Leu Glu Phe	Ala Thr Leu Phe	Ser Gly Gln Gly
50	55	60	
Ser Lys Val Thr	Ile Ile Asp Arg	Gly Glu Leu	Pro Leu Lys Asn Phe
65	70	75	80
Asp Arg Glu Val	Ala Glu Leu	Ala Lys Thr	Asp Leu Glu Ala Arg Gly
85	90	95	
Ile Thr Phe Leu	Asn Asn Ala Glu	Leu Thr Gly Phe	Ser Gly Asp Leu
100	105	110	
Thr Ile Ala Leu	Lys Asp His Asp	Leu Leu Ala Asp	Ala Ala Leu Phe
115	120	125	
Ala Ser Ala Asp	Ala Arg His Arg	Arg Ala Arg	Pro
130	135	140	
<210> 197			
<211> 612			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(589)			
<223> RXA01054			
<400> 197			
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ccttgaacag gcgggcatca aaacaggcac gcgtggggag gtg ctt gtc gac gcc 115			
Val Leu Val Asp Ala			
1 5			
cac ctc cgg acc aac atc gac ggc atc ttc gct gta ggt gat gtc aat 163			
His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala Val Gly Asp Val Asn			
10 15 20			
ggc ggc ccg cag ttt acc tac gtg tcc tac gat gac cac cgc att gtg 211			
Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp Asp His Arg Ile Val			
25 30 35			
ctg gat caa cta gcc gga aca ggt aag aaa tcc att gca cac cga ctg 259			
Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser Ile Ala His Arg Leu			
40 45 50			
atc ccc acc acc acg ttc atc gaa ccg ccg tta tcc acc atc ggt gac 307			

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Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu Ser Thr Ile Gly Asp
  55                      60                      65
aac act gaa ggg gaa aat gtg gtg gtg aaa aag gcc ttg att gca gat 355
Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys Ala Leu Ile Ala Asp
  70                      75                      80                      85

atg ccg atc gtt ccc cga cca gag att att aac caa cct cac ggt atg 403
Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn Gln Pro His Gly Met
                      90                      95                      100

gtg aag ttt ttc gtc gac aag caa tct gat gcg ctg ctc ggc gcg acc 451
Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala Leu Leu Gly Ala Thr
                      105                      110                      115

ttg tac tgc gcc gac tcc cag gag ctc atc aac acc gtg gcg ctt gcc 499
Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn Thr Val Ala Leu Ala
                      120                      125                      130

atg cgg cat ggc gtc acc gcc tcc gag ctt ggc gac ggc atc tac acc 547
Met Arg His Gly Val Thr Ala Ser Glu Leu Gly Asp Gly Ile Tyr Thr
                      135                      140                      145

cac ccc gcc acc tcg gag atc ttc aac caa tta ttg ggc agt 589
His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu Leu Gly Ser
                      150                      155                      160

taacgcagcg gatcgaacgg ctt 612

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<210> 198

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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Val Leu Val Asp Ala His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala
  1                      5                      10                      15

Val Gly Asp Val Asn Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp
                      20                      25                      30

Asp His Arg Ile Val Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser
                      35                      40                      45

Ile Ala His Arg Leu Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu
                      50                      55                      60

Ser Thr Ile Gly Asp Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys
                      65                      70                      75                      80

Ala Leu Ile Ala Asp Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn
                      85                      90                      95

Gln Pro His Gly Met Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala
                      100                      105                      110

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Leu Leu Gly Ala Thr Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn
 115 120 125

Thr Val Ala Leu Ala Met Arg His Gly Val Thr Ala Ser Glu Leu Gly
 130 135 140

Asp Gly Ile Tyr Thr His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu
 145 150 155 160

Leu Gly Ser

<210> 199

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> RXN03123

<400> 199

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tggcttttgt gctgcacgag ccgctggggc ccgcctcggc gtg ggc gac gcg ctg 115
 Val Gly Asp Ala Leu
 1 5

cga ggc cgg gga aag cct gaa gtc atg cgc tac cca gga att ccg ttc 163
 Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr Pro Gly Ile Pro Phe
 10 15 20

gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc tta ggc gat ctc 211
 Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu Gly Asp Leu
 25 30 35

acc tct tac cca gcg atc tgc tgc att ctg gag acc ttg gac ggt gaa 259
 Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu Asp Gly Glu
 40 45 50

atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt gat tac acc 307
 Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu Asp Tyr Thr
 55 60 65

ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg att tcc aac 355
 Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp Ile Ser Asn
 70 75 80 85

gaa caa tcc ttc att gat cac atc gct gac acg gat tac acc gat ttt 403
 Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr Thr Asp Phe
 90 95 100

tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt gcg gcc aag aag 451
 Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg Ala Ala Lys Lys
 105 110 115

cat ctg cag acc cac gcc ggc atg ccc aag acg cac atg aac gcg caa 499
 His Leu Gln Thr His Ala Gly Met Pro Lys Thr His Met Asn Ala Gln
 120 125 130

ggc tat tgg aac aag ggc aga gcc atg ggt aaa agc aat taaaagattt 548
 Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys Ser Asn
 135 140 145

ttgcttatcg acg 561

<210> 200

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Val Gly Asp Ala Leu Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr
 1 5 10 15

Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu
 20 25 30

Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu
 35 40 45

Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp
 50 55 60

Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala
 65 70 75 80

Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr
 85 90 95

Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr
 100 105 110

Arg Ala Ala Lys Lys His Leu Gln Thr His Ala Gly Met Pro Lys Thr
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His Met Asn Ala Gln Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys
 130 135 140

Ser Asn
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<210> 201

<211> 736

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> FRXA00993

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 Met Gly Lys Gly Phe
 1 5

acc ggc gct att ttg acc gtc atg ggc gtg aaa tcg cat atc gcc acc 163
 Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys Ser His Ile Ala Thr
 10 15 20

acc acg gga aaa acc gtg atc aat gac cgc atg gtg acc att cat ttt 211
 Thr Thr Gly Lys Thr Val Ile Asn Asp Arg Met Val Thr Ile His Phe
 25 30 35

cat tcc gag acg ctg ctc aac acg gaa ggt gaa gtc ccc ggc gat tgg 259
 His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu Val Pro Gly Asp Trp
 40 45 50

ctg cgt ctg tgg ttc ccg cac gag agc cga cct gga aag ctc tac caa 307
 Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro Gly Lys Leu Tyr Gln
 55 60 65

cgc gcc tac acc ttg acc aac gtg gat gcc gat gcc ggt acc ttt gac 355
 Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp Ala Gly Thr Phe Asp
 70 75 80 85

ctg gct ttt gtg ctg cac gag ccg ctg ggg ccc gcc tcg gcg tgg gcg 403
 Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro Ala Ser Ala Trp Ala
 90 95 100

acg cgc tgc gag gcc ggg gaa agc ctg gaa gtc atg cgc tac cca gga 451
 Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val Met Arg Tyr Pro Gly
 105 110 115

att ccg ttc gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc cta 499
 Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu
 120 125 130

ggc gat ctc acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg 547
 Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu
 135 140 145

gac ggt gaa atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt 595
 Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu
 150 155 160 165

gat tac acc ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg 643
 Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp
 170 175 180

att tcc aac gaa caa tcc ttc att gat cac atc gct gac acg gat tac 691
 Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr
 185 190 195

736

acc gat ttt tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt
 Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg
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<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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 20 25 30

Val Thr Ile His Phe His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu
 35 40 45

Val Pro Gly Asp Trp Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro
 50 55 60

Gly Lys Leu Tyr Gln Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp
 65 70 75 80

Ala Gly Thr Phe Asp Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro
 85 90 95

Ala Ser Ala Trp Ala Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val
 100 105 110

Met Arg Tyr Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg
 115 120 125

Gly Phe Leu Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser
 130 135 140

Ile Leu Glu Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile
 145 150 155 160

Ala His Asp Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His
 165 170 175

Ile Thr Ala Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile
 180 185 190

Ala Asp Thr Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser
 195 200 205

Ser Glu Thr Arg
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<210> 203

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(709)

<223> RXA01051

<400> 203

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taacagtgaa cacacaggcc atccccctag ggttggccat atg tca acc att cac 115
                                         Met Ser Thr Ile His
                                         1 5

gcc tcc gga atc cag gct cca caa gtg cca cac ggt tcc cac cat gcc 163
Ala Ser Gly Ile Gln Ala Pro Gln Val Pro His Gly Ser His His Ala
                        10 15 20

ccg cca caa aag gac gaa tca gtg aag aag agc ttc aat gcc tct tct 211
Pro Pro Gln Lys Asp Glu Ser Val Lys Lys Ser Phe Asn Ala Ser Ser
                        25 30 35

tta ctg ttc gcg ttt tcc ttc ggc gtg tac ctg gtg ctg ctt gtg atg 259
Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu Val Leu Leu Val Met
                        40 45 50

atg aca ctt ctt aaa agt cgc ctt tct tta ggc gga ctg tgg aac aca 307
Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly Gly Leu Trp Asn Thr
                        55 60 65

gaa gca cac caa tac aga tcc atc gac tta gag ctt ttc aac ggc ttt 355
Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu Leu Phe Asn Gly Phe
                        70 75 80 85

gct gat cca cca att tgg tgg ggg cct tgg acc aac act ttt ggc aac 403
Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr Asn Thr Phe Gly Asn
                        90 95 100

atc gca ctg ttc atg cca ttt ggg ttt ttc ctg tac aaa atg ctc cgt 451
Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu Tyr Lys Met Leu Arg
                        105 110 115

aga ttc aac cat cga ttc ccc ttc gta gaa acc atc ctg ttt gcc agc 499
Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr Ile Leu Phe Ala Ser
                        120 125 130

gtc acc agc ctc agt atc gaa gtt ctg caa tgg gtg ttt gct att gga 547
Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp Val Phe Ala Ile Gly
                        135 140 145

tat tca gat gtc gat gac ctg ttg ttt aat acg atc ggc gga ctc att 595
Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr Ile Gly Gly Leu Ile
                        150 155 160 165

gga gca tcc gta gca gcg ctt gtc tcg ctt aaa tcc tcc aag gta gtc 643
Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys Ser Ser Lys Val Val
                        170 175 180

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agc gga atc atc atg ggc ggt tca cta tct gtg atg gcg atg atg atg 691
 Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val Met Ala Met Met Met
 185 190 195

tat tca agt ttt atc gcc tagaaggttt cagcagttcc gct 732
 Tyr Ser Ser Phe Ile Ala
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<210> 204

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

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Phe Asn Ala Ser Ser Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu
 35 40 45

Val Leu Leu Val Met Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly
 50 55 60

Gly Leu Trp Asn Thr Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu
 65 70 75 80

Leu Phe Asn Gly Phe Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr
 85 90 95

Asn Thr Phe Gly Asn Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu
 100 105 110

Tyr Lys Met Leu Arg Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr
 115 120 125

Ile Leu Phe Ala Ser Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp
 130 135 140

Val Phe Ala Ile Gly Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr
 145 150 155 160

Ile Gly Gly Leu Ile Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys
 165 170 175

Ser Ser Lys Val Val Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val
 180 185 190

Met Ala Met Met Met Tyr Ser Ser Phe Ile Ala
 195 200

<210> 205

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXN01873

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 Met Ser Gln Ala Ile
 1 5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc caa gaa ggc atc 163
 Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
 10 15 20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc 211
 Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala
 25 30 35

gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt 259
 Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu
 40 45 50

ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg 307
 Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu
 55 60 65

acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg 355
 Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala
 70 75 80 85

tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca 403
 Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser
 90 95 100

ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat 451
 Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn
 105 110 115

att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct 499
 Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala
 120 125 130

ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc 547
 Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro
 135 140 145

aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc 595
 Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val
 150 155 160 165

ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act 643

Gly	Gly	Leu	Thr	Gly	Arg	Met	Ile	Pro	Ala	Gly	Leu	Leu	Glu	Val	Thr		
				170					175					180			
cat	tgg	caa	aac	gca	ctg	ctg	gga	agt	tct	atc	gct	gcg	ctg	atc	ttc	691	
His	Trp	Gln	Asn	Ala	Leu	Leu	Gly	Ser	Ser	Ile	Ala	Ala	Leu	Ile	Phe		
			185					190					195				
ggc	gta	atc	atg	gtg	gtg	ttg	ctt	ccc	aag	cag	cgg	aaa	ttc	cag	ccg	739	
Gly	Val	Ile	Met	Val	Val	Leu	Leu	Pro	Lys	Gln	Arg	Lys	Phe	Gln	Pro		
		200					205					210					
aag	aat	atc	aat	ctg	cgc	cat	gag	att	tcg	gcg	atg	gct	gct	cat	tgg	787	
Lys	Asn	Ile	Asn	Leu	Arg	His	Glu	Ile	Ser	Ala	Met	Ala	Ala	His	Trp		
	215					220				225							
cgg	aat	cct	cgt	ttg	gcg	ttg	ctt	ttt	ggg	act	gcg	ttt	ttg	ggc	atg	835	
Arg	Asn	Pro	Arg	Leu	Ala	Leu	Leu	Phe	Gly	Thr	Ala	Phe	Leu	Gly	Met		
230					235					240					245		
ggg	act	ttt	gtg	tcg	ctg	tac	aac	tat	ttg	ggg	ttc	cgc	atg	att	gat	883	
Gly	Thr	Phe	Val	Ser	Leu	Tyr	Asn	Tyr	Leu	Gly	Phe	Arg	Met	Ile	Asp		
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cag	ttt	ggg	ctg	agt	gaa	gtg	ctg	gtt	ggg	gcg	gtg	ttc	atc	atg	tat	931	
Gln	Phe	Gly	Leu	Ser	Glu	Val	Leu	Val	Gly	Ala	Val	Phe	Ile	Met	Tyr		
			265					270					275				
ctg	gcc	ggg	acc	tgg	agt	tcc	acc	cag	gcg	ggg	gcg	ttg	agg	gag	aag	979	
Leu	Ala	Gly	Thr	Trp	Ser	Ser	Thr	Gln	Ala	Gly	Ala	Leu	Arg	Glu	Lys		
		280					285					290					
atc	ggc	aat	ggg	tca	acg	gtt	att	ttc	ttg	agt	ctg	acg	atg	atc	gcg	1027	
Ile	Gly	Asn	Gly	Ser	Thr	Val	Ile	Phe	Leu	Ser	Leu	Thr	Met	Ile	Ala		
	295					300					305						
tcg	atg	gca	ctg	atg	ggg	att	aat	aat	ttg	tgg	gtc	acg	ttg	gtt	gcc	1075	
Ser	Met	Ala	Leu	Met	Gly	Ile	Asn	Asn	Leu	Trp	Val	Thr	Leu	Val	Ala		
310					315					320					325		
ctg	ttt	gtg	ttt	acc	gcg	gca	ttt	ttc	gca	ctg	cat	tcc	agt	gct	tcg	1123	
Leu	Phe	Val	Phe	Thr	Ala	Ala	Phe	Phe	Ala	Leu	His	Ser	Ser	Ala	Ser		
			330					335						340			
gga	tgg	atc	gga	atc	atc	gca	acg	aag	gat	cgc	gcg	gaa	gcc	tcc	agc	1171	
Gly	Trp	Ile	Gly	Ile	Ile	Ala	Thr	Lys	Asp	Arg	Ala	Glu	Ala	Ser	Ser		
			345					350					355				
atg	tat	ttg	ttc	tgt	tat	tac	gtg	gga	tcc	tcg	gtg	att	ggg	tgg	gtt	1219	
Met	Tyr	Leu	Phe	Cys	Tyr	Tyr	Val	Gly	Ser	Ser	Val	Ile	Gly	Trp	Val		
		360					365					370					
tct	gga	ttc	gcg	ttt	acg	cat	ttg	ccg	tgg	ttg	gcg	ttc	att	ggc	tgg	1267	
Ser	Gly	Phe	Ala	Phe	Thr	His	Leu	Pro	Trp	Leu	Ala	Phe	Ile	Gly	Trp		
	375					380					385						
ttg	att	ctg	ctt	ctt	tgc	gga	gtg	ctg	gcg	att	tgt	gtg	acg	ctg	gca	1315	
Leu	Ile	Leu	Leu	Leu	Cys	Gly	Val	Leu	Ala	Ile	Cys	Val	Thr	Leu	Ala		

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 Arg Leu Ala Arg Asn Ala Asn
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<210> 206
 <211> 412
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 206
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 Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys
 35 40 45
 Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
 50 55 60
 Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
 65 70 75 80
 Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
 85 90 95
 Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
 100 105 110
 Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
 115 120 125
 Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
 130 135 140
 Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
 145 150 155 160
 Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
 165 170 175
 Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
 180 185 190
 Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
 195 200 205
 Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
 210 215 220
 Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
 225 230 235 240

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<210> 207
<211> 1215
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA01873
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                                     Met Ser Gln Ala Ile
                                     1                               5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc cac gaa ggc atc 163
Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
                                     10                               15                               20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc 211

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Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala	
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gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt	259
Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu	
40 45 50	
ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg	307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu	
55 60 65	
acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg	355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala	
70 75 80 85	
tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca	403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser	
90 95 100	
ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat	451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn	
105 110 115	
att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct	499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala	
120 125 130	
ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc	547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro	
135 140 145	
aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc	595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val	
150 155 160 165	
ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act	643
Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr	
170 175 180	
cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc	691
His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe	
185 190 195	
ggc gta atc atg gtg gtg ttg ctt ccc aag cag cgg aaa ttc cag ccg	739
Gly Val Ile Met Val Val Leu Leu Pro Lys Gln Arg Lys Phe Gln Pro	
200 205 210	
aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg	787
Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp	
215 220 225	
cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg	835
Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met	
230 235 240 245	
ggt act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat	883
Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp	

	250	255	260	
cag ttt ggg ctg agt gaa gtg ctg gtt ggt gcg gtg ttc atc atg tat				931
Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala Val Phe Ile Met Tyr				
	265	270	275	
ctg gcc ggg acc tgg agt tcc acc cag gcg ggt gcg ttg agg gag aag				979
Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly Ala Leu Arg Glu Lys				
	280	285	290	
atc ggc aat ggg tca acg gtt att ttc ttg agt ctg acg atg atc gcg				1027
Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser Leu Thr Met Ile Ala				
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tcg atg gca ctg atg ggg att aat aat ttg tgg gtc acg ttg gtt gcc				1075
Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp Val Thr Leu Val Ala				
	310	315	320	325
ctg ttt gtg ttt acc gcg gca ttt ttc gca ctg cat tcc agt gct tcg				1123
Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu His Ser Ser Ala Ser				
	330	335	340	
gga tgg atc gga atc atc gca acg aag gat cgc gcg gaa gcc tcc agc				1171
Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg Ala Glu Ala Ser Ser				
	345	350	355	
atg tat ttg ttc tgt gaa tac taggatacctc ggtgattggt tgg				1215
Met Tyr Leu Phe Cys Glu Tyr				
	360			

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<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys				
	35	40	45	
Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro				
	50	55	60	
Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu				
	65	70	75	80
Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg				
	85	90	95	
Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu				
	100	105	110	

Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
 115 120 125
 Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
 130 135 140
 Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
 145 150 155 160
 Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
 165 170 175
 Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
 180 185 190
 Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
 195 200 205
 Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
 210 215 220
 Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
 225 230 235 240
 Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
 245 250 255
 Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
 260 265 270
 Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
 275 280 285
 Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
 290 295 300
 Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
 305 310 315 320
 Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
 325 330 335
 His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
 340 345 350
 Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Glu Tyr
 355 360

<210> 209

<211> 1572

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1549)

<223> RXN00034

<400> 209

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 Met Ser Tyr Thr Ser
 1 5

ttt aaa ggc gat gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc 163
 Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
 10 15 20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg 211
 Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
 25 30 35

gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg 259
 Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
 40 45 50

gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc 307
 Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
 55 60 65

gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt 355
 Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
 70 75 80 85

aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc 403
 Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala
 90 95 100

acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg 451
 Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
 105 110 115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt 499
 Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
 120 125 130

act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt 547
 Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
 135 140 145

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
 Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
 150 155 160 165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
 Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
 170 175 180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
 Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
 185 190 195

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt	739
Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser	
200 205 210	
gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg	787
Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp	
215 220 225	
acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt	835
Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu	
230 235 240 245	
gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac	883
Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp	
250 255 260	
ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac	931
Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn	
265 270 275	
ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt	979
Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val	
280 285 290	
cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc	1027
Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser	
295 300 305	
atc ggc ttc gca gcc ttt gtc atc ctt ttc att cga gtt gga gaa aag	1075
Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile Arg Val Gly Glu Lys	
310 315 320 325	
gcc atg cag aaa gtt ggc gcc cga gca gtg atc atc acc gct ggc atc	1123
Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile Ile Thr Ala Gly Ile	
330 335 340	
ttg gta gcg acc gcg acc gcc ctc cta atg atc acc gcg gtc agc gag	1171
Leu Val Ala Thr Ala Thr Ala Leu Met Ile Thr Ala Val Ser Glu	
345 350 355	
tca acg tac atc gtc atc tcc ctc gcc ggc ttc tcc ctt tat ggc ctt	1219
Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe Ser Leu Tyr Gly Leu	
360 365 370	
ggc ctc gga ctc ttc gcc acc cca gtc acc gat act gcg ctt gga aca	1267
Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp Thr Ala Leu Gly Thr	
375 380 385	
ctt ccc aaa gac cgt acc ggc gct ggt gca ggt gta ttc aag atg tcc	1315
Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly Val Phe Lys Met Ser	
390 395 400 405	
tct tcc ctc ggc gca gca ctc ggc atc gca atc tcc act tca gtg ttc	1363
Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile Ser Thr Ser Val Phe	
410 415 420	

ctc gca ctt cgc gac ggc acc tcc atc aac tcc gac gtc gca ctc gcc 1411
 Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser Asp Val Ala Leu Ala
 425 430 435

gga aca gtt tca ctt ggc atc aac gtt gta ttc gca gca aca gcc acc 1459
 Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe Ala Ala Thr Ala Thr
 440 445 450

atc acc gca gca gtc ctt att cca aaa gcc gct ggc aaa gtc tca caa 1507
 Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala Gly Lys Val Ser Gln
 455 460 465

acc agc atc acc ctt cct gag cca gct atc gct gta aaa atc 1549
 Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala Val Lys Ile
 470 475 480

taaaacttca ccaggacaga taa 1572

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 210
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Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
 35 40 45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
 50 55 60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
 65 70 75 80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
 85 90 95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
 100 105 110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115 120 125

Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
 130 135 140

Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
 145 150 155 160

Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
 165 170 175

Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
 180 185 190
 Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195 200 205
 Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210 215 220
 Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225 230 235 240
 Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
 245 250 255
 Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260 265 270
 Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275 280 285
 Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290 295 300
 Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile
 305 310 315 320
 Arg Val Gly Glu Lys Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile
 325 330 335
 Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu Met Ile
 340 345 350
 Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe
 355 360 365
 Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp
 370 375 380
 Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly
 385 390 395 400
 Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile
 405 410 415
 Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser
 420 425 430
 Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe
 435 440 445
 Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala
 450 455 460
 Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala
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Val Lys Ile

<210> 211

<211> 1045

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> FRXA02273

<400> 211

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				Met	Ser	Tyr	Thr	Ser	
				1				5	

ttt	aaa	ggc	gat	gat	aaa	gcc	ctc	atc	ggc	ata	ggt	tta	tca	ggt	ctc	163
Phe	Lys	Gly	Asp	Asp	Lys	Ala	Leu	Ile	Gly	Ile	Val	Leu	Ser	Val	Leu	
			10					15						20		

aca	ttt	tgg	ctt	ttt	gct	cag	tca	acc	cta	aat	atc	ggc	cca	gat	atg	211
Thr	Phe	Trp	Leu	Phe	Ala	Gln	Ser	Thr	Leu	Asn	Ile	Gly	Pro	Asp	Met	
			25					30					35			

gca	act	gat	tta	ggg	atg	agc	gat	ggc	acc	atg	aac	ata	gct	gtc	gtg	259
Ala	Thr	Asp	Leu	Gly	Met	Ser	Asp	Gly	Thr	Met	Asn	Ile	Ala	Val	Val	
		40				45					50					

gcc	gcc	gcg	tta	ttc	tgt	gga	aca	ttt	atc	gtc	gca	gcc	ggc	ggc	atc	307
Ala	Ala	Ala	Leu	Phe	Cys	Gly	Thr	Phe	Ile	Val	Ala	Ala	Gly	Gly	Ile	
	55					60					65					

gca	gat	gtc	ttt	ggc	cga	gta	cga	atc	atg	atg	att	ggc	aac	atc	ctt	355
Ala	Asp	Val	Phe	Gly	Arg	Val	Arg	Ile	Met	Met	Ile	Gly	Asn	Ile	Leu	
	70				75				80						85	

aac	atc	ctg	gga	tct	ctc	ctc	atc	gcc	acg	gca	acg	act	tct	tta	gcc	403
Asn	Ile	Leu	Gly	Ser	Leu	Leu	Ile	Ala	Thr	Ala	Thr	Thr	Ser	Leu	Ala	
			90						95					100		

acc	caa	atg	gtg	atc	acc	ggc	cga	gtt	ctc	caa	gga	ctg	gca	gca	gcg	451
Thr	Gln	Met	Val	Ile	Thr	Gly	Arg	Val	Leu	Gln	Gly	Leu	Ala	Ala	Ala	
			105					110					115			

gcc	atc	atg	tct	gca	tcc	cta	gca	tta	gtt	aag	aca	tat	tgg	tta	ggt	499
Ala	Ile	Met	Ser	Ala	Ser	Leu	Ala	Leu	Val	Lys	Thr	Tyr	Trp	Leu	Gly	
		120					125					130				

act	gac	cgc	caa	cga	gca	gtc	tcc	att	tgg	tcc	att	ggg	tca	tgg	ggg	547
Thr	Asp	Arg	Gln	Arg	Ala	Val	Ser	Ile	Trp	Ser	Ile	Gly	Ser	Trp	Gly	
	135					140					145					


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ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
150                      155                      160                      165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
170                      175                      180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
185                      190                      195

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt 739
Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
200                      205                      210

gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg 787
Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
215                      220                      225

acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt 835
Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
230                      235                      240                      245

gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac 883
Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
250                      255                      260

ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac 931
Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
265                      270                      275

ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt 979
Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val
280                      285                      290

cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc 1027
Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
295                      300                      305

atc ggc ttc gca gcc ttt 1045
Ile Gly Phe Ala Ala Phe
310                      315

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<210> 212

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
  20              25              30

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Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
 35 40 45
 Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
 50 55 60
 Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
 65 70 75 80
 Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
 85 90 95
 Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
 100 105 110
 Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115 120 125
 Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
 130 135 140
 Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
 145 150 155 160
 Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
 165 170 175
 Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
 180 185 190
 Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195 200 205
 Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210 215 220
 Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225 230 235 240
 Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
 245 250 255
 Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260 265 270
 Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275 280 285
 Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290 295 300
 Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe
 305 310 315

<210> 213

<211> 826
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXN03075

<400> 213

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agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
                               Val Ala Lys Phe Leu
                               1      5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
                10                15                20

gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat 211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
                25                30                35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc 259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
                40                45                50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca 307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
                55                60                65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag 355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
                70                75                80                85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat 403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
                90                95                100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat 451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
                105                110                115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg 499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
                120                125                130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg 547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
                135                140                145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act 595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
                150                155                160                165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag 643
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Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
 170 175 180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc 691
 Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
 185 190 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc 739
 Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
 200 205 210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc 787
 Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
 215 220 225

ttc ggt tgc ttc atc gct gcc ggt atg ccg ctg atc tct 826
 Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
 230 235 240

<210> 214

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
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Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
 20 25 30

Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala

165 170 175
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
 210 215 220
 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240
 Ile Ser

<210> 215
 <211> 826
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> FRXA02907

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 Val Ala Lys Phe Leu 5
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 tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
 Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala 20
 10 15
 gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat 211
 Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr 35
 25 30
 gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc 259
 Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val 50
 40 45
 acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca 307
 Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala 65
 55 60
 aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag 355
 Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys 85
 70 75 80
 acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat 403
 Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp

90										95					100					
gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat	451																			
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp																				
105 110 115																				
cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg	499																			
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu																				
120 125 130																				
gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg	547																			
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser																				
135 140 145																				
att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act	595																			
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr																				
150 155 160 165																				
ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag	643																			
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys																				
170 175 180																				
gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc	691																			
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val																				
185 190 195																				
tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc	739																			
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr																				
200 205 210																				
tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc	787																			
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr																				
215 220 225																				
ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct	826																			
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser																				
230 235 240																				

<210> 216

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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			20					25					30		

Leu	Ala	Gly	Leu	Tyr	Ala	Lys	Pro	Thr	Ser	Ser	Ser	Phe	Ser	Ile	Pro
		35					40					45			

Gly	Leu	Asp	Ser	Val	Thr	Thr	Met	Glu	Lys	Met	Gln	Glu	Arg	Phe	Pro
	50					55					60				

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80
 Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95
 Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110
 Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125
 Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140
 Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160
 Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
 210 215 220
 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240
 Ile Ser

<210> 217

<211> 2313

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2290)

<223> RXA00479

<400> 217

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cttagaacta acctttacgc cttaacgga agtgaatttg atg tct act agc atc 115
 Met Ser Thr Ser Ile
 1 5

aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc 163
 Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
 10 15 20

ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc	211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val	
25 30 35	
ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag	259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln	
40 45 50	
acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag	307
Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln	
55 60 65	
ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg	355
Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met	
70 75 80 85	
gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa	403
Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu	
90 95 100	
gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc	451
Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser	
105 110 115	
cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc	499
Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro	
120 125 130	
ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag	547
Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu	
135 140 145	
acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga	595
Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly	
150 155 160 165	
ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat	643
Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp	
170 175 180	
ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc	691
Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val	
185 190 195	
atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt	739
Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala Val Leu Ala Thr Ser	
200 205 210	
ttg ttt gcg ctg act gta gct cta ttg gtg gtg tgg tgg cta gct aag	787
Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val Trp Trp Leu Ala Lys	
215 220 225	
tgg gac atc ctg ctg ctt tcg ggt cag act caa ggc atc ctc ttc att	835
Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln Gly Ile Leu Phe Ile	
230 235 240 245	

ctg gtc att ggc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu Leu Tyr Val Ala Arg 250 255 260	883
ttc cgt gaa gag tta cgc gtt caa caa gat aaa ggg ata gcc aca ggg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys Gly Ile Ala Thr Gly 265 270 275	931
aaa gcc atc cgg gca tcg gtg gaa ccc att ctt gcc tcg ggc agc act Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu Ala Ser Gly Ser Thr 280 285 290	979
gtt att gcg ggc ctc ctt tgt ttg cta ttt agt gat ttg aaa tct aac Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser Asp Leu Lys Ser Asn 295 300 305	1027
tcc acg cta ggt cca gta gct tcg gtg ggc att att ttt gca atg ctt Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu 310 315 320 325	1075
tct gct ctt act ctg cta cca gcc ctg ctg ttt gta ttc ggt cgg gtg Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val 330 335 340	1123
gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala 345 350 355	1171
aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu 360 365 370	1219
gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu 375 380 385	1267
ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser 390 395 400 405	1315
caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln 410 415 420	1363
gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile 425 430 435	1411
atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn 440 445 450	1459
aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser 455 460 465	1507
ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt	1555

286

695

700

705

gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag 2275
 Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
 710 715 720 725

aag cag cct cag cta tgacacacca aaattcgct ctc 2313
 Lys Gln Pro Gln Leu
 730

<210> 218

<211> 730

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

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Arg Leu Met Arg Ile Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu
 20 25 30

Val Gly Ala Gly Val Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val
 35 40 45

Ser Ser Asn Ser Gln Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr
 50 55 60

Gln Val Gln Glu Gln Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro
 65 70 75 80

Ala Ile Val Val Met Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile
 85 90 95

Thr Gln Leu Asn Glu Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val
 100 105 110

Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
 115 120 125

Gln Val Phe Val Pro Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val
 130 135 140

Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
 145 150 155 160

Thr Tyr Val Thr Gly Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala
 165 170 175

Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val
 180 185 190

Leu Val Ile Leu Val Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala
 195 200 205

Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val

210	215	220
Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln 225 230 235 240		
Gly Ile Leu Phe Ile Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu 245 250 255		
Leu Tyr Val Ala Arg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys 260 265 270		
Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu 275 280 285		
Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser 290 295 300		
Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile 305 310 315 320		
Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe 325 330 335		
Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro 340 345 350		
Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser 355 360 365		
Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser 370 375 380		
Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys 385 390 395 400		
Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala 405 410 415		
Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly 420 425 430		
Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala 435 440 445		
Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser 450 455 460		
Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val 465 470 475 480		
Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln 485 490 495		
Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala 500 505 510		
Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile		

515					520					525					
Ser	Ala	Val	Val	Gly	Gly	Val	Thr	Ala	Thr	Ser	Val	Asp	Thr	Asn	Asp
530						535					540				
Ala	Ser	Ile	His	Asp	Arg	Asn	Leu	Ile	Ile	Pro	Ile	Val	Leu	Leu	Val
545					550					555					560
Ile	Leu	Val	Ile	Leu	Met	Leu	Leu	Leu	Arg	Ser	Ile	Val	Ala	Pro	Leu
				565					570					575	
Leu	Leu	Val	Val	Thr	Thr	Val	Val	Ser	Phe	Ala	Thr	Ala	Leu	Gly	Val
				580				585					590		
Ala	Ala	Leu	Leu	Phe	Asn	His	Val	Phe	Ser	Phe	Pro	Gly	Ala	Asp	Pro
				595				600					605		
Ala	Val	Pro	Leu	Tyr	Gly	Phe	Val	Phe	Leu	Val	Ala	Leu	Gly	Ile	Asp
	610					615					620				
Tyr	Asn	Ile	Phe	Leu	Val	Thr	Arg	Ile	Arg	Glu	Glu	Thr	Lys	Thr	His
625						630					635				640
Gly	Thr	Arg	Leu	Gly	Ile	Leu	Arg	Gly	Leu	Thr	Val	Thr	Gly	Gly	Val
				645					650					655	
Ile	Thr	Ser	Ala	Gly	Val	Val	Leu	Ala	Ala	Thr	Phe	Ala	Ala	Leu	Tyr
				660					665					670	
Val	Ile	Pro	Ile	Leu	Phe	Leu	Ala	Gln	Ile	Ala	Phe	Ile	Val	Ala	Phe
				675				680					685		
Gly	Val	Leu	Ile	Asp	Thr	Leu	Leu	Val	Arg	Ala	Phe	Leu	Val	Pro	Ala
	690					695					700				
Leu	Phe	Tyr	Asp	Ile	Gly	Pro	Lys	Ile	Trp	Trp	Pro	Ser	Lys	Leu	Ser
705						710					715				720
Asn	Gln	Lys	Tyr	Gln	Lys	Gln	Pro	Gln	Leu						
				725					730						

<210> 219

<211> 983

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(960)

<223> RXN03124

<400> 219

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1				5					10				15			

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag	96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln	
20 25 30	
act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc	144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg	
35 40 45	
acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc	192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct	240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc	288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc	336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca	384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg	432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac	480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	
145 150 155 160	
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc	528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr	
165 170 175	
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc	576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr	
180 185 190	
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc	624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly	
195 200 205	
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag	672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu	
210 215 220	
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac	720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn	
225 230 235 240	
act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc	768

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
 245 250 255
 gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc 816
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
 260 265 270
 gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg 864
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
 275 280 285
 ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt 912
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
 290 295 300
 acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc 960
 Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
 305 310 315 320
 tgatcgtttt ggttctagcg ttc 983

 <210> 220
 <211> 320
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
 20 25 30
 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35 40 45
 Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
 50 55 60
 Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65 70 75 80
 Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
 85 90 95
 Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
 100 105 110
 Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
 115 120 125
 Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
 130 135 140
 Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
 145 150 155 160

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Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
      165                      170                      175

Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
      180                      185                      190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
      195                      200                      205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
      210                      215                      220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
      225                      230                      235                      240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
      245                      250                      255

Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
      260                      265                      270

Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
      275                      280                      285

Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
      290                      295                      300

Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
      305                      310                      315                      320

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<210> 221
 <211> 762
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(762)
 <223> FRXA01180

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Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
  1                      5                      10                      15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag   96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
      20                      25                      30

act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc   144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
      35                      40                      45

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acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc 192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
    50                      55                      60

act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct 240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
    65                      70                      75                      80

ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc 288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
                      85                      90                      95

att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc 336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
    100                      105                      110

ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca 384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
    115                      120                      125

cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg 432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
    130                      135                      140

atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac 480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
    145                      150                      155                      160

ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc 528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
                      165                      170                      175

aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc 576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
                      180                      185                      190

gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc 624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
    195                      200                      205

cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag 672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
    210                      215                      220

gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac 720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
    225                      230                      235                      240

act gat ggt gtg aag aat gct cag atc act cag acc acg gag 762
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu
                      245                      250

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<210> 222

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

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Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
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Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
 20           25           30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35           40           45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
 50           55           60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65           70           75           80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
 85           90           95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
100           105           110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
115           120           125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
130           135           140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145           150           155           160

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
165           170           175

Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
180           185           190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
195           200           205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
210           215           220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225           230           235           240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu
245           250

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<210> 223

<211> 393

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02586

<400> 223

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gatgccacca tcatccgcgt gctgcttgtc ccccgccgtg atg cac ctg ctt cgc 115
                                         Met His Leu Leu Arg
                                         1 5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163
Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
                        10 15 20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211
Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
                        25 30 35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259
Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
                        40 45 50

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307
Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
                        55 60 65

gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355
Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
                        70 75 80 85

ctt gag gat cta gat taaatctatg cgaggatttt tca 393
Leu Glu Asp Leu Asp
                        90

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<210> 224

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

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Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys
 1 5 10 15

Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
 20 25 30

Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
 35 40 45

Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
 50 55 60

Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
 65 70 75 80

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Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
85 90

<210> 225

<211> 2214

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2191)

<223> RXA02587

<400> 225

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ttgttatcca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg 115
Val Phe Ser Lys Trp
1 5

ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc 163
Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
10 15 20

gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac 211
Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp
25 30 35

cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct 259
Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Ser Thr Ala
40 45 50

gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat 307
Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp
55 60 65

gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca 355
Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr Ser Phe Asp Asp Ala
70 75 80 85

gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac 403
Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp Gly Leu Ile Glu Asn
90 95 100

aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat 451
Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr Phe Asp Thr Arg Asn
105 110 115

caa aat ctc ctc agc aaa gac ggc acc caa acc ttt gca gct ctc ggg 499
Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr Phe Ala Ala Leu Gly
120 125 130

ctc aaa ggt gac ggc gag caa acg ctg aag gac ttc cgg gag att gaa 547
Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp Phe Arg Glu Ile Glu
135 140 145

gat cag ctc cat ccg gac aac ctt gcc ggt ggc gtc acc act gag gtc Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly Val Thr Thr Glu Val 150 155 160 165	595
gcg ggt gcc acc gct gta gcc gac gca ctc gat gag ggc atg gct ggc Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp Glu Gly Met Ala Gly 170 175 180	643
gat att tca cgc gcc gaa gtt ttt gcg ctg cct ttc gtg gct atc ttg Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro Phe Val Ala Ile Leu 185 190 195	691
ctg ctc atc gtg ttt ggc tca gtt gtt gcc gcg gcg atg cca ttg atc Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala Met Pro Leu Ile 200 205 210	739
gtg ggc att ttg tcc atc ttg ggt tcg ctg ggc atc ttg gca att ttg Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly Ile Leu Ala Ile Leu 215 220 225	787
gct gga ttc ttc cag gtc aac gta ttt gca caa tct gtt gtg acc ctt Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln Ser Val Val Thr Leu 230 235 240 245	835
ctg ggc ttg ggt ctt gcc att gac tat ggc tta ttc atg gtc tct cgt Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu Phe Met Val Ser Arg 250 255 260	883
ttc cgt gag gaa atg gat aag ggc acc ccg gtt gaa cag gct gtt gcc Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val Glu Gln Ala Val Ala 265 270 275	931
acc act acg gcg acc gcg ggt aag act gtg gtg ttc tct gca gcg atg Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val Phe Ser Ala Ala Met 280 285 290	979
gtg gct gtg gcg ctg tcc ggg ttg ttt gtt ttc cca cag gct ttc ttg Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe Pro Gln Ala Phe Leu 295 300 305	1027
aag tcg gtg gca ttc ggt gcg att tcc gcg gtt ggc ctt gct gct ttg Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val Gly Leu Ala Ala Leu 310 315 320 325	1075
atg tcg gtg acg gtg ttg ccg tcg ctg ttc agc atg ttg ggt aag aat Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser Met Leu Gly Lys Asn 330 335 340	1123
atc gat aag tgg agt ttg cgt cgc act gct cga aca gcg cgc cgt ttg Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg Thr Ala Arg Arg Leu 345 350 355	1171
gaa gac acc att tgg tac cgc gtg ccg gca tgg gca atg cgc cat gcc Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala 360 365 370	1219

aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg	1267
Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val	
375 380 385	
ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca	1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro	
390 395 400 405	
cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt	1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe	
410 415 420	
ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac	1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp	
425 430 435	
aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga	1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly	
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ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg	1507
Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr	
455 460 465	
gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg	1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val	
470 475 480 485	
gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc	1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile	
490 495 500	
ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa	1651
Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu	
505 510 515	
aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc	1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu	
520 525 530	
atg gca ttg gta ttt ggt tcg gtg att ttg ccg gcg aag gcc atc atc	1747
Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile	
535 540 545	
atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg	1795
Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met	
550 555 560 565	
ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca	1843
Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro	
570 575 580	
ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt	1891
Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu	
585 590 595	
tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc	1939

Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131
Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179
Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
680 685 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg 2214
Thr Arg Leu Arg
695

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<211> 697

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

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20 25 30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
35 40 45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
50 55 60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
65 70 75 80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
85 90 95

Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
100 105 110

Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
115 120 125

Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
 130 135 140
 Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly
 145 150 155 160
 Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
 165 170 175
 Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
 180 185 190
 Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
 195 200 205
 Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
 210 215 220
 Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
 225 230 235 240
 Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
 245 250 255
 Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
 260 265 270
 Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
 275 280 285
 Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
 290 295 300
 Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
 305 310 315 320
 Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
 325 330 335
 Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
 340 345 350
 Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
 355 360 365
 Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
 370 375 380
 Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
 385 390 395 400
 Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
 405 410 415
 Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
 420 425 430

Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
 435 440 445
 Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr
 450 455 460
 Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
 465 470 475 480
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
 485 490 495
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
 610 615 620
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
 625 630 635 640
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
 645 650 655
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
 660 665 670
 Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
 675 680 685
 Arg Gln Leu Val Gly Thr Arg Leu Arg
 690 695

<210> 227

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN03042

<400> 227

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tcgcctcggc gacgtcctgg ttccttacgt tctgacggtt ttg gtt cta gcg ttc 115
 Leu Val Leu Ala Phe
 1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
 Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
 10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
 Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
 25 30 35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
 Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
 40 45 50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
 Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
 55 60 65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355
 Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
 70 75 80 85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
 Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
 90 95 100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
 Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
 105 110 115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499
 Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
 120 125 130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
 Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
 135 140 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
 Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
 150 155 160 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643
 Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu
 170 175 180

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691
 Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
 185 190 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729
 Val Gly Val Gly Ala
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<210> 228

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

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 20 25 30
 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45
 Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60
 Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80
 Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95
 Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110
 Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125
 Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140
 Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160
 Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175
 Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190
 Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

<210> 229

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA02893

<400> 229

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				Leu Val Leu Ala Phe	
				1 5	

ctc gtg ctg ttg ctc gtg ttc	cgg tcc att tgg gtc cca ttg atc gcg	163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala		
10 15 20		

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg	211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val	
25 30 35	

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca	259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro	
40 45 50	

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg	307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu	
55 60 65	

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc	355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe	
70 75 80 85	

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac	403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His	
90 95 100	

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc	451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe	
105 110 115	

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt	499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe	
120 125 130	

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg	547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met	
135 140 145	

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta	595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu	
150 155 160 165	

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag	643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu	

170	175	180	
ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat			691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn			
185	190	195	
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Val Gly Val Gly Ala			
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20	25	30	
Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile			
35	40	45	
Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly			
50	55	60	
Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg			
65	70	75	80
Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser			
85	90	95	
Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile			
100	105	110	
Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile			
115	120	125	
Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe			
130	135	140	
Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp			
145	150	155	160
Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val			
165	170	175	
Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu			
180	185	190	
Glu Leu Lys Glu Asn Val Gly Val Gly Ala			
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<222> (101)..(1582)  
<223> RXA01616
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				Met	Thr	Ser	Glu	Thr									
				1				5									
tta	cag	gcg	caa	gcg	cct	acg	aaa	acc	caa	cgt	tgg	gct	ttc	ctc	gcc	163	
Leu	Gln	Ala	Gln	Ala	Pro	Thr	Lys	Thr	Gln	Arg	Trp	Ala	Phe	Leu	Ala		
			10						15					20			
ggt	atc	agc	ggt	ggt	ctc	ttt	ctg	atc	ggt	gta	gac	aac	tgc	att	ctc	211	
Val	Ile	Ser	Gly	Gly	Leu	Phe	Leu	Ile	Gly	Val	Asp	Asn	Ser	Ile	Leu		
			25					30					35				
tac	acc	gca	ctc	cct	ctg	ctg	cgt	gaa	cag	ctc	gca	gcc	tcc	gaa	acc	259	
Tyr	Thr	Ala	Leu	Pro	Leu	Leu	Arg	Glu	Gln	Leu	Ala	Ala	Ser	Glu	Thr		
		40					45					50					
caa	gcg	ttg	tgg	atc	atc	aac	gca	tat	ccc	ctg	ctc	atg	gcg	ggc	ctt	307	
Gln	Ala	Leu	Trp	Ile	Ile	Asn	Ala	Tyr	Pro	Leu	Leu	Met	Ala	Gly	Leu		
	55					60					65						
cgt	ttg	ggt	gcc	ggc	act	ttg	ggt	gac	aaa	aac	ggc	cac	cgc	cgg	atg	355	
Arg	Leu	Gly	Ala	Gly	Thr	Leu	Gly	Asp	Lys	Asn	Gly	His	Arg	Arg	Met		
	70				75					80					85		
ttc	ctc	atg	ggc	ttg	agc	att	ttc	gga	atc	gct	tca	ctt	ggt	gct	gcg	403	
Phe	Leu	Met	Gly	Leu	Ser	Ile	Phe	Gly	Ile	Ala	Ser	Leu	Gly	Ala	Ala		
				90					95					100			
ttt	gct	cca	act	gcg	tgg	gct	ctt	gtt	gct	gcg	aga	gct	ttc	ctt	ggc	451	
Phe	Ala	Pro	Thr	Ala	Trp	Ala	Leu	Val	Ala	Ala	Arg	Ala	Phe	Leu	Gly		
		105					110						115				
atc	ggt	gcg	gca	acg	atg	atg	cct	gca	acc	ttg	gct	ctg	atc	cgc	att	499	
Ile	Gly	Ala	Ala	Thr	Met	Met	Pro	Ala	Thr	Leu	Ala	Leu	Ile	Arg	Ile		
		120					125					130					
cg	ttt	gag	gat	gag	cgt	gag	cgc	aac	act	gca	att	ggt	att	tgg	ggt	547	
Thr	Phe	Glu	Asp	Glu	Arg	Glu	Arg	Asn	Thr	Ala	Ile	Gly	Ile	Trp	Gly		
	135					140					145						
cc	gtg	gca	att	ctt	ggc	gct	gcg	gca	ggc	ccg	atc	att	ggt	ggt	gcg	595	
er	Val	Ala	Ile	Leu	Gly	Ala	Ala	Ala	Gly	Pro	Ile	Ile	Gly	Gly	Ala		
	50				155				160					165			

ctg ttg gaa ttc ttc tgg tgg ggt tgc gtt ttc ctc att aac gtt ccg	643
Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe Leu Ile Asn Val Pro	
170 175 180	
gtg gct gtt atc gcg ttg atc gct acg ctt ttt gtg gcg ccg gcc aat	691
Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe Val Ala Pro Ala Asn	
185 190 195	
atc gcg aat ccg tct aag cat tgg gat ttc ttg tgc tgc ttc tat gcg	739
Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu Ser Ser Phe Tyr Ala	
200 205 210	
ctg ctc aca ctt gct ggg ttg atc atc acg atc aag gaa tct gtg aat	787
Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile Lys Glu Ser Val Asn	
215 220 225	
act gca cgc cat atg cct ctt ctt ttg ggt gca gtc atc atg ttg atc	835
Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala Val Ile Met Leu Ile	
230 235 240 245	
att ggt gcg gtg ttg ttt agc agt cgt cag aag aag atc gag gag cca	883
Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys Lys Ile Glu Glu Pro	
250 255 260	
ctt cta gat ctg tgc ttg ttc cgt aat cgc ctt ttc tta ggc ggt gtg	931
Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu Phe Leu Gly Gly Val	
265 270 275	
gtt gct gcg ggc atg gcg atg ttt act gtg tcc ggt ttg gaa atg act	979
Val Ala Ala Gly Met Ala Met Phe Thr Val Ser Gly Leu Glu Met Thr	
280 285 290	
acc tgc cag cgt ttc cag ttg tct gtg ggt ttc act cca ctt gag gct	1027
Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe Thr Pro Leu Glu Ala	
295 300 305	
ggt ttg ctc atg atc cca gct gca ttg ggt agc ttc ccg atg tct att	1075
Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser Phe Pro Met Ser Ile	
310 315 320 325	
atc ggt ggt gca aac ctg cat cgt tgg ggc ttc aaa ccg ctg atc agt	1123
Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe Lys Pro Leu Ile Ser	
330 335 340	
ggt ggt ttt gct gcc act gcc gtt ggc atc gcc ctg tgt att tgg ggc	1171
Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala Leu Cys Ile Trp Gly	
345 350 355	
gcg act cat act gat ggt ttg ccg ttt ttc atc gcg ggt cta ttc ttc	1219
Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile Ala Gly Leu Phe Phe	
360 365 370	
atg ggc gcg ggt gct ggt tgc gta atg tct gtg tct tcc act gcg att	1267
Met Gly Ala Gly Ala Gly Ser Val Met Ser Val Ser Ser Thr Ala Ile	
375 380 385	
atc ggt tcc gcg ccg gtg cgt aag gct ggc atg gcg tgc tgc atc gaa	1315

Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met Ala Ser Ser Ile Glu
 390 395 400 405

gag gtc tct tat gag ttc ggc acg ctg ttg tct gtc gcg att ttg ggt 1363
 Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser Val Ala Ile Leu Gly
 410 415 420

agc ttg ttc cca ttc ttc tac tcg ctg cat gcc ccg gca gag gtt gcg 1411
 Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala Pro Ala Glu Val Ala
 425 430 435

gat aac ttc tcg gcg ggt gtt cac cac gcg att gat ggc gat gcg gcg 1459
 Asp Asn Phe Ser Ala Gly Val His His Ala Ile Asp Gly Asp Ala Ala
 440 445 450

cgt gca tct ttg gac acc gca tac att aac gtg ttg atc att gcc cta 1507
 Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val Leu Ile Ile Ala Leu
 455 460 465

gta tgc gca gta gcg gct gct ctg atc agc agt tac ctt ttc cgc gga 1555
 Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser Tyr Leu Phe Arg Gly
 470 475 480 485

aat ccg aag gga gcc aat aat gcg cac tagtaaaaaa gagatgattc 1602
 Asn Pro Lys Gly Ala Asn Asn Ala His
 490

tgc 1605

<210> 232

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

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Trp Ala Phe Leu Ala Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val
 20 25 30

Asp Asn Ser Ile Leu Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu
 35 40 45

Ala Ala Ser Glu Thr Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu
 50 55 60

Leu Met Ala Gly Leu Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn
 65 70 75 80

Gly His Arg Arg Met Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala
 85 90 95

Ser Leu Gly Ala Ala Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala
 100 105 110

Arg Ala Phe Leu Gly Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu
 115 120 125
 Ala Leu Ile Arg Ile Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala
 130 135 140
 Ile Gly Ile Trp Gly Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro
 145 150 155 160
 Ile Ile Gly Gly Ala Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe
 165 170 175
 Leu Ile Asn Val Pro Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe
 180 185 190
 Val Ala Pro Ala Asn Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu
 195 200 205
 Ser Ser Phe Tyr Ala Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile
 210 215 220
 Lys Glu Ser Val Asn Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala
 225 230 235 240
 Val Ile Met Leu Ile Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys
 245 250 255
 Lys Ile Glu Glu Pro Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu
 260 265 270
 Phe Leu Gly Gly Val Val Ala Ala Gly Met Ala Met Phe Thr Val Ser
 275 280 285
 Gly Leu Glu Met Thr Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe
 290 295 300
 Thr Pro Leu Glu Ala Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser
 305 310 315 320
 Phe Pro Met Ser Ile Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe
 325 330 335
 Lys Pro Leu Ile Ser Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala
 340 345 350
 Leu Cys Ile Trp Gly Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile
 355 360 365
 Ala Gly Leu Phe Phe Met Gly Ala Gly Ala Gly Ser Val Met Ser Val
 370 375 380
 Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
 385 390 395 400
 Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
 405 410 415

Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
 420 425 430

Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
 435 440 445

Asp Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
 450 455 460

Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser
 465 470 475 480

Tyr Leu Phe Arg Gly Asn Pro Lys Gly Ala Asn Asn Ala His
 485 490

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1477)
 <223> RXA01666

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 Val Ser Thr Phe His
 1 5

aaa gtt ttg atc aac acc atg atc tcc aac gtc acc act gga ttt ctg 163
 Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val Thr Thr Gly Phe Leu
 10 15 20

ttc ttt gcc gtg gtg ttt tgg atg tat ctt tcc act ggc aac gtc gca 211
 Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser Thr Gly Asn Val Ala
 25 30 35

ctg acc ggc atc gtc agt gga att tac atg ggt ttg atc gcc gtt tgt 259
 Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly Leu Ile Ala Val Cys
 40 45 50

tcc atc ttt ttc gga acc gtt gtt gat cac aat cgc aag aag tcc gtc 307
 Ser Ile Phe Phe Gly Thr Val Val Asp His Asn Arg Lys Lys Ser Val
 55 60 65

atg ctg ttt tcc agc gtc acc aca ctc gtg ttt tat tgt ctc agt gcc 355
 Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe Tyr Cys Leu Ser Ala
 70 75 80 85

ctg gtg tgg gtg ttt tgg ctg gag gaa gac ggc ctg agc atc gga aat 403
 Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly Leu Ser Ile Gly Asn
 90 95 100

acc gcc ctg tgg gtg ttc gtt tct ttc atc ctc atc gga tca atc gtg	451
Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu Ile Gly Ser Ile Val	
105 110 115	
gaa cac atg cgc aac atc gca ctg tcc acc gtg gtc acg ctg ttg gtt	499
Glu His Met Arg Asn Ile Ala Leu Ser Thr Val Val Thr Leu Leu Val	
120 125 130	
cct gaa gct gaa cgc gac aaa gca aac ggc ctg gta gga gcc gtg caa	547
Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu Val Gly Ala Val Gln	
135 140 145	
ggg gtt gga ttt tta gtc acc agc gtc att gct ggt tcc gcc atc ggg	595
Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala Gly Ser Ala Ile Gly	
150 155 160 165	
ttc ttg ggc atg gaa atc acc ctg tgg atc tgc ctt ggg ctc tca ctt	643
Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys Leu Gly Leu Ser Leu	
170 175 180	
gtc gcg ctg ctg cac ctg ctg ccg att cgc gtc gac gaa ccg gaa atc	691
Val Ala Leu Leu His Leu Leu Pro Ile Arg Val Asp Glu Pro Glu Ile	
185 190 195	
atc acc caa gaa gac gca cag cct act gtt tct gac gat tca gtt ccc	739
Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser Asp Asp Ser Val Pro	
200 205 210	
aca cct acc tcc gat ttg gcg atc gtg tcc aaa ggc atc gac cta aaa	787
Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys Gly Ile Asp Leu Lys	
215 220 225	
gga tca atg aaa atc atc ctg agt gtt ccg gga ctg ctc gcg ctt gtg	835
Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly Leu Leu Ala Leu Val	
230 235 240 245	
ttg ttt gcg tcc ttc aac aac ctc atc ggc ggc gtg tac tcc gca ctc	883
Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly Val Tyr Ser Ala Leu	
250 255 260	
atg gac cct tac ggc ctg gaa ctt ttc agc cca cag ctg tgg ggg cta	931
Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro Gln Leu Trp Gly Leu	
265 270 275	
ctg ctt gga ctc acc agc ctc ggc ttc atc gtt ggt ggt gct gtg atc	979
Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val Gly Gly Ala Val Ile	
280 285 290	
tcc aaa act ggc ttg ggc aaa aac cct gtg cgc acc ttg ctg ctg gtt	1027
Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg Thr Leu Leu Leu Val	
295 300 305	
aat gtt ggt gtg gct ttt gtt ggc atg tta ttt gcc att cgc gaa tgg	1075
Asn Val Gly Val Ala Phe Val Gly Met Leu Phe Ala Ile Arg Glu Trp	
310 315 320 325	
tgg tgg ctc tac atc ctg ggc att ttc atc ttc atg gct atc acc cca	1123

Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe Met Ala Ile Thr Pro
 330 335 340
 gct gcc gaa gcc gca gaa caa acc atc ctt caa cga gtc gtc cca ttc 1171
 Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln Arg Val Val Pro Phe
 345 350 355
 cgc caa caa ggc cgc gta ttt gga cta gcc atg gca gtg gaa atg gca 1219
 Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met Ala Val Glu Met Ala
 360 365 370
 gcc aac ccg ctc tcc aca gtg atc gtg gcg att ttg gcc gaa gcc tac 1267
 Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile Leu Ala Glu Ala Tyr
 375 380 385
 ctc att cca tgg atg gct ggc ccc ggc gcg gac acc atc tgg ggc gtg 1315
 Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp Thr Ile Trp Gly Val
 390 395 400 405
 atc ctc ggc gag ggt aaa gct cgc ggc atg gca ctg atg ttc ctc gca 1363
 Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala Leu Met Phe Leu Ala
 410 415 420
 tca ggt gcc atc atg ttg gtt gtc gtg ctg ttg gca ttc atg tcg agg 1411
 Ser Gly Ala Ile Met Leu Val Val Val Leu Leu Ala Phe Met Ser Arg
 425 430 435
 tcc tac cgg aaa ctc agc cag tac tac gcc acc acc agc caa gac att 1459
 Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr Thr Ser Gln Asp Ile
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 Ala Gly Ala Ala Glu Lys
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 <213> Corynebacterium glutamicum
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 Thr Gly Asn Val Ala Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly
 35 40 45
 Leu Ile Ala Val Cys Ser Ile Phe Phe Gly Thr Val Val Asp His Asn
 50 55 60
 Arg Lys Lys Ser Val Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe
 65 70 75 80

Tyr Cys Leu Ser Ala Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly
 85 90 95
 Leu Ser Ile Gly Asn Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu
 100 105 110
 Ile Gly Ser Ile Val Glu His Met Arg Asn Ile Ala Leu Ser Thr Val
 115 120 125
 Val Thr Leu Leu Val Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu
 130 135 140
 Val Gly Ala Val Gln Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala
 145 150 155 160
 Gly Ser Ala Ile Gly Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys
 165 170 175
 Leu Gly Leu Ser Leu Val Ala Leu Leu His Leu Leu Pro Ile Arg Val
 180 185 190
 Asp Glu Pro Glu Ile Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser
 195 200 205
 Asp Asp Ser Val Pro Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys
 210 215 220
 Gly Ile Asp Leu Lys Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly
 225 230 235 240
 Leu Leu Ala Leu Val Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly
 245 250 255
 Val Tyr Ser Ala Leu Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro
 260 265 270
 Gln Leu Trp Gly Leu Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val
 275 280 285
 Gly Gly Ala Val Ile Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg
 290 295 300
 Thr Leu Leu Leu Val Asn Val Gly Val Ala Phe Val Gly Met Leu Phe
 305 310 315 320
 Ala Ile Arg Glu Trp Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe
 325 330 335
 Met Ala Ile Thr Pro Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln
 340 345 350
 Arg Val Val Pro Phe Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met
 355 360 365
 Ala Val Glu Met Ala Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile
 370 375 380

Leu Ala Glu Ala Tyr Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp
385 390 395 400

Thr Ile Trp Gly Val Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala
405 410 415

Leu Met Phe Leu Ala Ser Gly Ala Ile Met Leu Val Val Val Leu Leu
420 425 430

Ala Phe Met Ser Arg Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr
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Thr Ser Gln Asp Ile Ala Gly Ala Ala Glu Lys
450 455

<210> 235

<211> 1521

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1498)

<223> RXA00062

<400> 235

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tcactgttgc gttttcttgc tgccatcaaa aattagtcac atg att tta agc atc 115
Met Ile Leu Ser Ile
1 5

gtc ctt ttg ggc tac ttc atg att ctg ctt gac acc tcc atc gtc att 163
Val Leu Leu Gly Tyr Phe Met Ile Leu Leu Asp Thr Ser Ile Val Ile
10 15 20

acg ggt cta cct gcc atc ggc agt gaa ctt ggc atc gat ccc gtg cac 211
Thr Gly Leu Pro Ala Ile Gly Ser Glu Leu Gly Ile Asp Pro Val His
25 30 35

ctg tca tgg gtg cag agt tcc tac aca tta gtc ttc ggc gca ctt ctt 259
Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val Phe Gly Ala Leu Leu
40 45 50

ctg ctg gga gct cgt gcc ggt gat atc ttc ggc cga aag aaa gtg ctc 307
Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly Arg Lys Lys Val Leu
55 60 65

tac att ggt ctc gcg ttg ttt gcg gct tca tcg ttg gca att gcg ctt 355
Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser Leu Ala Ile Ala Leu
70 75 80 85

tct cca aat gct gcg gtc ctc att gga gca cgc gta gtt caa ggc gcg 403
Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg Val Val Gln Gly Ala
90 95 100

gga gct gcg att atc gct cca gcg aca ctt gcg ttg att act gag ttc	451
Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala Leu Ile Thr Glu Phe	
105 110 115	
ttc ccc gaa ggc cca gct cgc ctt cgt gct acc tct gct tat ggt gct	499
Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr Ser Ala Tyr Gly Ala	
120 125 130	
gtt gcc ggc atc ggt gtg gca gca ggc cta gtg atc ggc ggc gta ttt	547
Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val Ile Gly Gly Val Phe	
135 140 145	
gct gat ctt ttg tcg tgg cgc atc ggc ttc ttt atc aac gtc ccc atc	595
Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe Ile Asn Val Pro Ile	
150 155 160 165	
gcc gca gtg ttg gcc tac ata gtg cac aaa gcc att ccc gca acc ttc	643
Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala Ile Pro Ala Thr Phe	
170 175 180	
agc agg cct gga tca ctc gac atc ttc gga gca att acc tcc acg gca	691
Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala Ile Thr Ser Thr Ala	
185 190 195	
ggt atc gcc gcg gtg ctc tac gca att gtc cgc agc gcc gat tac agc	739
Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg Ser Ala Asp Tyr Ser	
200 205 210	
tgg aca gat ccg ttt gtg ttg att tcc ctc gtg ctg ggc atc gca gtg	787
Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val Leu Gly Ile Ala Val	
215 220 225	
ttc atc tgg ttc ctg cgc cat gaa tcc tca gcc aaa gaa cca ctt ctg	835
Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala Lys Glu Pro Leu Leu	
230 235 240 245	
ccc ctg ggg ctc ttt aaa aac cgc agg cga aac acc atc ttg gcc agc	883
Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn Thr Ile Leu Ala Ser	
250 255 260	
cgc ttt ctt ctg gtt ggc tcc gtg atg tca ttc ttc ttc ttt gcc acc	931
Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe Phe Phe Phe Ala Thr	
265 270 275	
cag ctg ttc cag gac acc atg gga atg aat gct ctc cag gca ggc ctt	979
Gln Leu Phe Gln Asp Thr Met Gly Met Asn Ala Leu Gln Ala Gly Leu	
280 285 290	
gcg ttc atg ccg cta tct ctg ctg cag ttt gcc agc gcc gcg atg gtg	1027
Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala Ser Ala Ala Met Val	
295 300 305	
cca cgg ctt tcc cga gca ggc gta tct gat tcc atg ctc acc gtc atc	1075
Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser Met Leu Thr Val Ile	
310 315 320 325	
ggt ttc gcc atc atg gtc atc ggc atg gca ggc ctc gca ttt gta cca	1123

Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly Leu Ala Phe Val Pro
 330 335 340

aac acg atg atc gcg ctg atc cta cca ata gtt ttg gtg gga ttt ggc 1171
 Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val Leu Val Gly Phe Gly
 345 350 355

caa ggc ttc gct ttc gga cca atg aca gct ctg gca gtt caa ggt gca 1219
 Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu Ala Val Gln Gly Ala
 360 365 370

ccg aag gac caa tcc ggc gcc gtt tct ggc ctg gtg aat tcc ctt cac 1267
 Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu Val Asn Ser Leu His
 375 380 385

caa atc ggc ggc acc ttc ggt ttg ggt gtg ttc tcc tcc ttg gct gtc 1315
 Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe Ser Ser Leu Ala Val
 390 395 400 405

gct gtc atc gga cat gat gca aca tca gag atg atc agc gac cgc gca 1363
 Ala Val Ile Gly His Asp Ala Thr Ser Glu Met Ile Ser Asp Arg Ala
 410 415 420

cac ttc gga ttc ttg ctc tcc acc gtg acg ctg acg ctg gcc acc atc 1411
 His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu Thr Leu Ala Thr Ile
 425 430 435

ttt gcg gtc aca ctg ctg aag cgc cac gaa acc cga aag agt agc gag 1459
 Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr Arg Lys Ser Ser Glu
 440 445 450

cgc cca acc cag ctc gtc gac gaa aag gca gtt acc tct tagtgcgctg 1508
 Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val Thr Ser
 455 460 465

cagcatccca gtt 1521

<210> 236

<211> 466

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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 20 25 30

Ile Asp Pro Val His Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val
 35 40 45

Phe Gly Ala Leu Leu Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly
 50 55 60

Arg Lys Lys Val Leu Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser

65	70	75	80
Leu Ala Ile Ala Leu Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg	85	90	95
Val Val Gln Gly Ala Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala	100	105	110
Leu Ile Thr Glu Phe Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr	115	120	125
Ser Ala Tyr Gly Ala Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val	130	135	140
Ile Gly Gly Val Phe Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe	145	150	155
Ile Asn Val Pro Ile Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala	165	170	175
Ile Pro Ala Thr Phe Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala	180	185	190
Ile Thr Ser Thr Ala Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg	195	200	205
Ser Ala Asp Tyr Ser Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val	210	215	220
Leu Gly Ile Ala Val Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala	225	230	235
Lys Glu Pro Leu Leu Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn	245	250	255
Thr Ile Leu Ala Ser Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe	260	265	270
Phe Phe Phe Ala Thr Gln Leu Phe Gln Asp Thr Met Gly Met Asn Ala	275	280	285
Leu Gln Ala Gly Leu Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala	290	295	300
Ser Ala Ala Met Val Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser	305	310	315
Met Leu Thr Val Ile Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly	325	330	335
Leu Ala Phe Val Pro Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val	340	345	350
Leu Val Gly Phe Gly Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu	355	360	365
Ala Val Gln Gly Ala Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu			

370

375

380

Val Asn Ser Leu His Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe
 385 390 395 400

Ser Ser Leu Ala Val Ala Val Ile Gly His Asp Ala Thr Ser Glu Met
 405 410 415

Ile Ser Asp Arg Ala His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu
 420 425 430

Thr Leu Ala Thr Ile Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr
 435 440 445

Arg Lys Ser Ser Glu Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val
 450 455 460

Thr Ser
 465

<210> 237

<211> 1584

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1561)

<223> RXA00215

<400> 237

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ccttttccag gcgccctcgt gcgtgaaaga ataactcaac gtg tct gac aaa aag 115
 Val Ser Asp Lys Lys
 1 5

cag gat cta aca tcc tcc gca gca ggt agt gct gca ccc caa acc aag 163
 Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala Ala Pro Gln Thr Lys
 10 15 20

gcc tac ccc gcc atg ccc ttg cct gaa aag caa gct tgg cca gct cta 211
 Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln Ala Trp Pro Ala Leu
 25 30 35

att gcc ttg tgc att ggg ttt ttc atg atc ctg ttg gat caa acc atc 259
 Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu Leu Asp Gln Thr Ile
 40 45 50

gtg gcc gtc tct acc cca gcg tta cag gca gac atg ggc gcg tcc tac 307
 Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp Met Gly Ala Ser Tyr
 55 60 65

aac gag gtc atc tgg gta acc tcg gtg tat ctc ctc act ttc gcg gtg 355
 Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu Leu Thr Phe Ala Val
 70 75 80 85

cca ctg ctt gtt act ggc cgt ttg ggc gac aag tac ggt ccg aaa aat	403
Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys Tyr Gly Pro Lys Asn	
90 95 100	
gtc tat gtc gca ggc atg gtt atc ttc aca gtg agc tct ttg gcc tgt	451
Val Tyr Val Ala Gly Met Val Ile Phe Thr Val Ser Ser Leu Ala Cys	
105 110 115	
ggc ttg gcc cca gac atg ttc acg ttg att atc gct cgt ggc gtt caa	499
Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile Ala Arg Gly Val Gln	
120 125 130	
ggc ttg ggc gca gcc ctt ttg act cca caa acc atg gca aca atc aac	547
Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr Met Ala Thr Ile Asn	
135 140 145	
cgc atc ttt gct ttt gag cgc cgc ggt gca gct ctt gga gtg tgg ggt	595
Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala Leu Gly Val Trp Gly	
150 155 160 165	
tct aca gct ggc ctt gca tcc cta gca gga ccg atc ctg ggt ggt gtc	643
Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro Ile Leu Gly Gly Val	
170 175 180	
atc acc gaa aac tgg ggt tgg caa tgg gtc ttc tac atc aac gtg ccc	691
Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe Tyr Ile Asn Val Pro	
185 190 195	
atc ggc gtg atc tcg gtg atc gca gta atg aag tac gtt cct gaa ttc	739
Ile Gly Val Ile Ser Val Ile Ala Val Met Lys Tyr Val Pro Glu Phe	
200 205 210	
cca ccg ctg acc cga ccg ctt gat ccg ctt tct atc gtg ttg tcc atc	787
Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser Ile Val Leu Ser Ile	
215 220 225	
gtg gcc gtg ttc ttc ctg gtg ttt gct ttc cag gaa ggc gaa ggc gct	835
Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln Glu Gly Glu Gly Ala	
230 235 240 245	
ggc tgg gcg gca tgg gtg tgg atc atg atc gta gcc gcc ttt gcg ctc	883
Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val Ala Ala Phe Ala Leu	
250 255 260	
ttt gcg tgg ttt atc tac caa caa agc agg gcc gag aaa tcc gga aac	931
Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala Glu Lys Ser Gly Asn	
265 270 275	
gat cct ctc gtc cca ctg gag att ttc aag ttt aga aac ttc agc ctc	979
Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe Arg Asn Phe Ser Leu	
280 285 290	
ggc aat atc tgc atc atg gcc atg gga ttc acc gtg gct ggt act cct	1027
Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr Val Ala Gly Thr Pro	
295 300 305	

ctg ccc atc atg ttg tac ttc cag caa gca cac gga atg aac gcc atg 1075
 Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His Gly Met Asn Ala Met
 310 315 320 325

gaa gcg ggt ttc atg atg gtg cct caa gct ctc atg gca gca gta ctg 1123
 Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu Met Ala Ala Val Leu
 330 335 340

tca cca ttt gtt gga aag ctg gtt gat cga tcc aac cct gga ctc atg 1171
 Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser Asn Pro Gly Leu Met
 345 350 355

gca gcc ctc ggt ttt agc aca gtg gct gtg tcc att gta ctg ctg tca 1219
 Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser Ile Val Leu Leu Ser
 360 365 370

atg gta atg att ttc gat acg ggt cta gtc tgg gca ctt gtt tcg atg 1267
 Met Val Met Ile Phe Asp Thr Gly Leu Val Trp Ala Leu Val Ser Met
 375 380 385

act ttg ctc ggc atc gga aac gcc ttt gtg tgg gca ccg aac tcg acc 1315
 Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp Ala Pro Asn Ser Thr
 390 395 400 405

tcc act atg cgc gac ctg cca cac aag ttc atg gga gcg ggc tct ggc 1363
 Ser Thr Met Arg Asp Leu Pro His Lys Phe Met Gly Ala Gly Ser Gly
 410 415 420

gtg ttc aat aca acc cgc caa tta ggt tca gtc atc ggc gcc gct gcc 1411
 Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val Ile Gly Ala Ala Ala
 425 430 435

atc ggc gcg gta atg cag att cga ctg gca gca ggc gat gag ggc gca 1459
 Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala Gly Asp Glu Gly Ala
 440 445 450

gct ttt ggt caa gca ctt cta ctt gcc gct gcg gtg ctg gtt atc ggc 1507
 Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala Val Leu Val Ile Gly
 455 460 465

att gtg gca tca acg atg gca gga aaa aat gca cac cca gcg ccg gta 1555
 Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala His Pro Ala Pro Val
 470 475 480 485

aag cct taaaggctcgc atgaatcctt cga 1584
 Lys Pro

<210> 238

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Val Ser Asp Lys Lys Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala
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Ala Pro Gln Thr Lys Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln
 20 25 30
 Ala Trp Pro Ala Leu Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu
 35 40 45
 Leu Asp Gln Thr Ile Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp
 50 55 60
 Met Gly Ala Ser Tyr Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu
 65 70 75 80
 Leu Thr Phe Ala Val Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys
 85 90 95
 Tyr Gly Pro Lys Asn Val Tyr Val Ala Gly Met Val Ile Phe Thr Val
 100 105 110
 Ser Ser Leu Ala Cys Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile
 115 120 125
 Ala Arg Gly Val Gln Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr
 130 135 140
 Met Ala Thr Ile Asn Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala
 145 150 155 160
 Leu Gly Val Trp Gly Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro
 165 170 175
 Ile Leu Gly Gly Val Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe
 180 185 190
 Tyr Ile Asn Val Pro Ile Gly Val Ile Ser Val Ile Ala Val Met Lys
 195 200 205
 Tyr Val Pro Glu Phe Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser
 210 215 220
 Ile Val Leu Ser Ile Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln
 225 230 235 240
 Glu Gly Glu Gly Ala Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val
 245 250 255
 Ala Ala Phe Ala Leu Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala
 260 265 270
 Glu Lys Ser Gly Asn Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe
 275 280 285
 Arg Asn Phe Ser Leu Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr
 290 295 300
 Val Ala Gly Thr Pro Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His
 305 310 315 320

Gly Met Asn Ala Met Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu
 325 330 335
 Met Ala Ala Val Leu Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser
 340 345 350
 Asn Pro Gly Leu Met Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser
 355 360 365
 Ile Val Leu Leu Ser Met Val Met Ile Phe Asp Thr Gly Leu Val Trp
 370 375 380
 Ala Leu Val Ser Met Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp
 385 390 395 400
 Ala Pro Asn Ser Thr Ser Thr Met Arg Asp Leu Pro His Lys Phe Met
 405 410 415
 Gly Ala Gly Ser Gly Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val
 420 425 430
 Ile Gly Ala Ala Ala Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala
 435 440 445
 Gly Asp Glu Gly Ala Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala
 450 455 460
 Val Leu Val Ile Gly Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala
 465 470 475 480
 His Pro Ala Pro Val Lys Pro
 485

<210> 239
 <211> 1455
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1432)
 <223> RXN03064

<400> 239
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 tgtcatcatc ttggctgtat tagtttttac agcctttgtc atg atg ttg aat gag 115
 Met Met Leu Asn Glu
 1 5
 act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att 163
 Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
 10 15 20
 gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211

Glu	Ala	Asn	Thr	Ala	Gln	Trp	Leu	Leu	Thr	Gly	Phe	Met	Leu	Thr	Met		
			25					30					35				
gct	gtg	gtt	ctt	cca	gct	act	ggg	tgg	atg	ttg	gaa	cgt	ttt	acc	act	259	
Ala	Val	Val	Leu	Pro	Ala	Thr	Gly	Trp	Met	Leu	Glu	Arg	Phe	Thr	Thr		
		40					45					50					
cgt	agt	gtg	ttt	att	ttc	gcc	acg	gtg	gtc	ttc	ctg	atc	ggg	act	gtg	307	
Arg	Ser	Val	Phe	Ile	Phe	Ala	Thr	Val	Val	Phe	Leu	Ile	Gly	Thr	Val		
	55					60					65						
acg	gct	gcg	ttg	tct	cct	act	ttt	gcg	att	atg	ctt	gca	gcc	cgc	gtc	355	
Thr	Ala	Ala	Leu	Ser	Pro	Thr	Phe	Ala	Ile	Met	Leu	Ala	Ala	Arg	Val		
	70				75					80					85		
gct	cag	gcg	att	ggg	acc	gct	gtg	atc	atg	ccg	ctg	ctg	atg	act	gtc	403	
Ala	Gln	Ala	Ile	Gly	Thr	Ala	Val	Ile	Met	Pro	Leu	Leu	Met	Thr	Val		
			90					95						100			
gcg	atg	acc	gtt	gtt	cct	cca	gag	cgc	cgt	ggc	gcc	gtc	atg	ggg	ttg	451	
Ala	Met	Thr	Val	Val	Pro	Pro	Glu	Arg	Arg	Gly	Ala	Val	Met	Gly	Leu		
			105					110					115				
att	gcg	gtc	gtg	atg	gcc	gtt	ggg	cct	gct	ctt	gga	cct	agt	gtg	gct	499	
Ile	Ala	Val	Val	Met	Ala	Val	Gly	Pro	Ala	Leu	Gly	Pro	Ser	Val	Ala		
		120					125					130					
ggg	ttc	gta	ctc	agc	ttg	tct	tcg	tgg	cac	gcg	att	ttc	tgg	gtc	atg	547	
Gly	Phe	Val	Leu	Ser	Leu	Ser	Ser	Trp	His	Ala	Ile	Phe	Trp	Val	Met		
	135					140					145						
gtt	ccg	ttg	gtg	ttt	gtg	gca	agc	ctg	atc	ggg	acc	ctg	cgt	ctg	acc	595	
Val	Pro	Leu	Val	Phe	Val	Ala	Ser	Leu	Ile	Gly	Thr	Leu	Arg	Leu	Thr		
	150				155					160					165		
aac	gtc	agt	gag	cct	aaa	aag	act	cct	ttg	gat	gtt	att	tcc	ttc	ctg	643	
Asn	Val	Ser	Glu	Pro	Lys	Lys	Thr	Pro	Leu	Asp	Val	Ile	Ser	Phe	Leu		
				170					175					180			
att	tcc	gca	gtg	gct	ttc	ggg	ggc	ctt	gtg	tac	gcc	ttg	agc	tcg	att	691	
Ile	Ser	Ala	Val	Ala	Phe	Gly	Gly	Leu	Val	Tyr	Ala	Leu	Ser	Ser	Ile		
		185						190					195				
ggc	atc	att	ttg	gaa	ggg	gac	aga	agc	gct	ttg	gtc	gtg	ttg	gct	gtc	739	
Gly	Ile	Ile	Leu	Glu	Gly	Asp	Arg	Ser	Ala	Leu	Val	Val	Leu	Ala	Val		
		200				205						210					
ggc	atc	att	gcg	ttg	gtg	gtg	ttt	gtg	tgg	cgc	cag	att	gcc	atg	ggg	787	
Gly	Ile	Ile	Ala	Leu	Val	Val	Phe	Val	Trp	Arg	Gln	Ile	Ala	Met	Gly		
	215					220					225						
aag	cag	gat	aag	gcg	ctg	ttg	gat	ctg	cgt	ccg	ttg	gcg	att	cgt	gag	835	
Lys	Gln	Asp	Lys	Ala	Leu	Leu	Asp	Leu	Arg	Pro	Leu	Ala	Ile	Arg	Glu		
	230				235					240					245		
tac	acc	att	ccg	ctg	gtt	gtg	ctt	ttg	acg	ctg	ttc	ggg	gcg	ctg	ctc	883	
Tyr	Thr	Ile	Pro	Leu	Val	Val	Leu	Leu	Thr	Leu	Phe	Gly	Ala	Leu	Leu		

	250	255	260	
ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc				931
Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val				
	265	270	275	
acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa				979
Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu				
	280	285	290	
ggt gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca				1027
Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro				
	295	300	305	
cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt				1075
Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe				
	310	315	320	325
gca ctg tcc acc gtc gat gag ttc gcc aac gtg tgg ttc atc atc ggc				1123
Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val Trp Phe Ile Ile Gly				
	330	335	340	
gta cac atc gtg ttc tcc atc ggc ctt gcg ctg ctg ttc acc cca ctg				1171
Val His Ile Val Phe Ser Ile Gly Leu Ala Leu Leu Phe Thr Pro Leu				
	345	350	355	
atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc				1219
Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly				
	360	365	370	
tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc				1267
Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr				
	375	380	385	
gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc				1315
Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile				
	390	395	400	405
gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca				1363
Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala				
	410	415	420	
ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc				1411
Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe				
	425	430	435	
ttt gta aag agg cca gcc cgc taagctaggt cgcatgatca gca				1455
Phe Val Lys Arg Pro Ala Arg				
	440			

<210> 240

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Met Leu Asn Glu Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met
 1 5 10 15
 Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
 20 25 30
 Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
 35 40 45
 Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
 50 55 60
 Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65 70 75 80
 Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
 85 90 95
 Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
 100 105 110
 Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
 115 120 125
 Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
 130 135 140
 Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
 145 150 155 160
 Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
 165 170 175
 Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
 180 185 190
 Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
 195 200 205
 Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
 210 215 220
 Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
 225 230 235 240
 Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
 245 250 255
 Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
 260 265 270
 Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
 275 280 285
 Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
 290 295 300

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
305 310 315 320

Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val
325 330 335

Trp Phe Ile Ile Gly Val His Ile Val Phe Ser Ile Gly Leu Ala Leu
340 345 350

Leu Phe Thr Pro Leu Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn
355 360 365

Met Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala
370 375 380

Gly Ala Ala Gly Thr Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser
385 390 395 400

Asn Asn Ala Leu Ile Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp
405 410 415

Gly Ala Asn Ser Ala Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala
420 425 430

Leu Ile Val Gly Phe Phe Val Lys Arg Pro Ala Arg
435 440

<210> 241

<211> 1093

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1093)

<223> FRXA00565

<400> 241

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tgtcatcatc ttggctgtat tagtttttac agcctttgtc atg atg ttg aat gag 115
Met Met Leu Asn Glu
1 5

act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att 163
Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
10 15 20

gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
25 30 35

gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
40 45 50

cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg	307
Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val	
55 60 65	
acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc	355
Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val	
70 75 80 85	
gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc	403
Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val	
90 95 100	
gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg	451
Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu	
105 110 115	
att gcg gtc gtg atg gcc gtt ggt cct gct ctt gga cct agt gtg gct	499
Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala	
120 125 130	
ggt ttc gta ctc agc ttg tct tcg tgg cac gcg att ttc tgg gtc atg	547
Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met	
135 140 145	
gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc	595
Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr	
150 155 160 165	
aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg	643
Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp Val Ile Ser Phe Leu	
170 175 180	
att tcc gca gtg gct ttc ggt ggc ctt gtg tac gcc ttg agc tcg att	691
Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr Ala Leu Ser Ser Ile	
185 190 195	
ggc atc att ttg gaa ggt gac aga agc gct ttg gtc gtg ttg gct gtc	739
Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu Val Val Leu Ala Val	
200 205 210	
ggc atc att gcg ttg gtg gtg ttt gtg tgg cgc cag att gcc atg ggt	787
Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg Gln Ile Ala Met Gly	
215 220 225	
aag cag gat aag gcg ctg ttg gat ctg cgt ccg ttg gcg att cgt gag	835
Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro Leu Ala Ile Arg Glu	
230 235 240 245	
tac acc att ccg ctg gtt gtg ctt ttg acg ctg ttc ggt gcg ctg ctc	883
Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu Phe Gly Ala Leu Leu	
250 255 260	
ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc	931
Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val	
265 270 275	
acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa	979

Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu
 280 285 290

ggt gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca 1027
 Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro
 295 300 305

cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt 1075
 Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe
 310 315 320 325

gca ctg tcc acc gtc gat 1093
 Ala Leu Ser Thr Val Asp
 330

<210> 242

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Met Leu Asn Glu Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met
 1 5 10 15

Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
 20 25 30

Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
 35 40 45

Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
 50 55 60

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65 70 75 80

Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
 85 90 95

Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
 100 105 110

Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
 115 120 125

Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
 130 135 140

Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
 145 150 155 160

Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
 165 170 175

Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
 180 185 190

Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
 195 200 205

Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
 210 215 220

Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
 225 230 235 240

Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
 245 250 255

Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
 260 265 270

Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
 275 280 285

Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
 290 295 300

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
 305 310 315 320

Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp
 325 330

<210> 243

<211> 380

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(357)

<223> FRXA02878

<400> 243

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gac aca tcg tgg ttc tca tcg gcc ctt gcg ctg ctg ttc acc cca ctg 96
 Asp Thr Ser Trp Phe Ser Ser Ala Leu Ala Leu Leu Phe Thr Pro Leu
 20 25 30

atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc 144
 Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
 35 40 45

tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc 192
 Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
 50 55 60

gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc 240

Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
65 70 75 80

gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca 288
Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
85 90 95

ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc 336
Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
100 105 110

ttt gta aag 'agg cca gcc cgc taagctaggt cgcatgatca gca 380
Phe Val Lys Arg Pro Ala Arg
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<210> 244

<211> 119

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Cys Leu Ser Thr Val Asp Glu Phe Ala Thr Cys Trp Ser Ser Phe Ala
1 5 10 15

Asp Thr Ser Trp Phe Ser Ser Ala Leu Ala Leu Leu Phe Thr Pro Leu
20 25 30

Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
35 40 45

Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
50 55 60

Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
65 70 75 80

Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
85 90 95

Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
100 105 110

Phe Val Lys Arg Pro Ala Arg
115

<210> 245

<211> 1533

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1510)

<223> RXA00648

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Val Val Thr Leu Ala
1 5

tca gct ggt atc act gtt tcc cta gcg cag acc ctg gtt att ccg atc 163
Ser Ala Gly Ile Thr Val Ser Leu Ala Gln Thr Leu Val Ile Pro Ile
10 15 20

att ggt cgg ttg ccc gag atc ttc aac acc acg gct gct aat gcc tct 211
Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr Ala Ala Asn Ala Ser
25 30 35

tgg atc att act gtg acg ctg ttg gtg ggc gca gtg gcg act cct gtg 259
Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala Val Ala Thr Pro Val
40 45 50

atg ggc agg ctt gca gat atg tac ggc aag aaa aag atg atg ctc atc 307
Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys Lys Met Met Leu Ile
55 60 65

tca ctt gtc ccg ttc att ctt gga tca gtg atc tgc gct gtg tcg gtg 355
Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile Cys Ala Val Ser Val
70 75 80 85

gat ttg att ccg atg atc atc ggc cgt ggt ttt cag ggg ctt ggc tct 403
Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe Gln Gly Leu Gly Ser
90 95 100

ggc ctg att cct ctt ggc att tct ctc atg cat gat ttg ttg ccc cgg 451
Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His Asp Leu Leu Pro Arg
105 110 115

gag aaa gca ggg tct gcc att gct ttg atg agt tct tcc atg ggc att 499
Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser Ser Ser Met Gly Ile
120 125 130

ggc ggt gca ctc ggt cta ccg ctg gct gct gct att gcc cag ttt gcg 547
Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala Ile Ala Gln Phe Ala
135 140 145

tcc tgg cgg gtg ctg ttc tgg ttc acc gct ctg gta gcg ctt aca gtt 595
Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu Val Ala Leu Thr Val
150 155 160 165

ggc gcg gtc att tgg aag gcg att cct gct aga ccc agg atc gtg agg 643
Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg Pro Arg Ile Val Arg
170 175 180

agt ggc ggc ttt gat tat ttc ggt gct ctc ggc ctt gca atg gga ctt 691
Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly Leu Ala Met Gly Leu
185 190 195

atc gca ttg ttg ctc gcg gtg tcc aag gga tca gaa tgg ggc tgg aga 739
Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser Glu Trp Gly Trp Arg

200	205	210	
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ggg tgg ggc tgg ttc gaa acc cgc cag aaa tcc cct ttg att gat ctg Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser Pro Leu Ile Asp Leu 230 235 240 245			835
cgc acc act att cgg gcg acc gtg ttg atg aca aat att gcg tcc atc Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr Asn Ile Ala Ser Ile 250 255 260			883
ctc atc ggt ttc acc atg tat gga atg aat ctg atc ctg cct cag gtc Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu Ile Leu Pro Gln Val 265 270 275			931
atg cag ctg cct gta att ctg ggc tac ggt cta ggc cag agc atg ctt Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu Gly Gln Ser Met Leu 280 285 290			979
cag atg ggc atc tgg ctg atc ccg atg ggt cta ggc atg atg ttg att Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu Gly Met Met Leu Ile 295 300 305			1027
tcg aat gca ggt gca gcc att agc gct gct cat ggt cct cgt gtg acg Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His Gly Pro Arg Val Thr 310 315 320 325			1075
ctg aca att gcg ggt gtt gtg atc gca gtc ggt tat gca ctt act gcc Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly Tyr Ala Leu Thr Ala 330 335 340			1123
aca gtg ttg ttc act atc ggc aac cgc aca ccg gga gga gat gca gac Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro Gly Gly Asp Ala Asp 345 350 355			1171
aac gca ctt att ttg acc acc ctg gtg ctg ttc tca gtg tgt agt ctc Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe Ser Val Cys Ser Leu 360 365 370			1219
gtg gtc ggt atc ggc att ggc ctg gca ttt ggt tcc atg cct gcc ttg Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly Ser Met Pro Ala Leu 375 380 385			1267
atc atg ggt gcc gta cca gcc acg gag aaa gcc gca gcg aat ggt ttc Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala Ala Ala Asn Gly Phe 390 395 400 405			1315
aac tct ctt atg cgt tca ctg ggc acc acc ggc tca tca gct gtc atc Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly Ser Ser Ala Val Ile 410 415 420			1363
ggg gca gtg ttg gcc gga atg atg agt ggc gga gta ccc acc tta ggg Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly Val Pro Thr Leu Gly 425 430 435			1411

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 Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys Ala Ala Leu Val Ala
 440 445 450

gcg gtc atc tcc tat ttc atc ccc acc aca acc act gtg gtg gaa gca 1507
 Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr Thr Val Val Glu Ala
 455 460 465

aaa taatcccggc agcgactcga cca 1533
 Lys
 470

<210> 246

<211> 470

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

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Ala Ala Asn Ala Ser Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala
 35 40 45

Val Ala Thr Pro Val Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys
 50 55 60

Lys Met Met Leu Ile Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile
 65 70 75 80

Cys Ala Val Ser Val Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe
 85 90 95

Gln Gly Leu Gly Ser Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His
 100 105 110

Asp Leu Leu Pro Arg Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser
 115 120 125

Ser Ser Met Gly Ile Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala
 130 135 140

Ile Ala Gln Phe Ala Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu
 145 150 155 160

Val Ala Leu Thr Val Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg
 165 170 175

Pro Arg Ile Val Arg Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly
 180 185 190

Leu Ala Met Gly Leu Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser

195	200	205
Glu Trp Gly Trp Arg Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala 210 215 220		
Leu Val Ile Leu Val Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser 225 230 235 240		
Pro Leu Ile Asp Leu Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr 245 250 255		
Asn Ile Ala Ser Ile Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu 260 265 270		
Ile Leu Pro Gln Val Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu 275 280 285		
Gly Gln Ser Met Leu Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu 290 295 300		
Gly Met Met Leu Ile Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His 305 310 315 320		
Gly Pro Arg Val Thr Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly 325 330 335		
Tyr Ala Leu Thr Ala Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro 340 345 350		
Gly Gly Asp Ala Asp Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe 355 360 365		
Ser Val Cys Ser Leu Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly 370 375 380		
Ser Met Pro Ala Leu Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala 385 390 395 400		
Ala Ala Asn Gly Phe Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly 405 410 415		
Ser Ser Ala Val Ile Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly 420 425 430		
Val Pro Thr Leu Gly Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys 435 440 445		
Ala Ala Leu Val Ala Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr 450 455 460		
Thr Val Val Glu Ala Lys 465 470		

<210> 247
 <211> 1770
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1747)

<223> RXN01320

<400> 247

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                                   Met Thr Ser Gln Val
                                   1 5
aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca 163
Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala
                                   10 15 20
cct tcg gcc cac acc tca gca cca tat ggt gca gca gca act gaa gaa 211
Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu
                                   25 30 35
gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc 259
Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala
                                   40 45 50
ctc atg ttg gcg atg ctt ctt agc tcc ttg ggt cag acc att ttc ggt 307
Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly Gln Thr Ile Phe Gly
                                   55 60 65
tct gcc ctg cca acg att gtt ggt gag ctt ggc ggc gtt aac cac atg 355
Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met
                                   70 75 80 85
acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct 403
Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro
                                   90 95 100
att ttc ggc aag ttg ggt gac cag ttt ggt cgc aaa tac ctc ttc atg 451
Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met
                                   105 110 115
ttt gcc atc gca ctg ttc gtg gtg ggt tcc atc atc ggt gct ttg gct 499
Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala
                                   120 125 130
cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc 547
Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala
                                   135 140 145
ggt ggt ggc ttg atg att ctt tct cag gca att acc gct gat gtc acc 595
Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr
                                   150 155 160 165
acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc 643
Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe
                                   170 175 180

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gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac	691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp	
185 190 195	
ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc	739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile	
200 205 210	
atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa	787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu	
215 220 225	
cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc	835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile	
230 235 240 245	
gcc acc acc gca ttt gtc ctc gca gtg acc tgg ggt ggc aat gaa tat	883
Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp Gly Gly Asn Glu Tyr	
250 255 260	
gag tgg gca tca cca atg atc atc ggt ttg ttc atc acg aca ttg gtc	931
Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe Ile Thr Thr Leu Val	
265 270 275	
gct gcg ata gtg ttc gtt ttc gtc gaa aag cgt gct gtt gac cca ctg	979
Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg Ala Val Asp Pro Leu	
280 285 290	
gtc ccc atg ggc ctt ttc tcg aac cgc aac ttc gtg ctc acc gcc gtc	1027
Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val Leu Thr Ala Val	
295 300 305	
gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc atc gcg tac atg	1075
Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr Ile Ala Tyr Met	
310 315 320 325	
cct acc tac ctg cag atg gtt cat ggt ctg aac cca acg caa gct ggt	1123
Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro Thr Gln Ala Gly	
330 335 340	
ctg atg ctg atc cca atg atg atc ggc ctg att ggt aca tcc act gtg	1171
Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly Thr Ser Thr Val	
345 350 355	
gtg ggc aac atc gtg tcc aag act ggc aag tac aag tgg tac cca ttc	1219
Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys Trp Tyr Pro Phe	
360 365 370	
atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg cta tcg acg ctg	1267
Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu Leu Ser Thr Leu	
375 380 385	
aca cct tcg gca agc ttg gct ctc att gga ctg tac ttc ttc gtc ttc	1315
Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr Phe Phe Val Phe	
390 395 400 405	

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 410 415 420
 aac tcc ttc cca atc acc atg gtt ggc acc gcg acc ggt tcc aac aac 1411
 Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr Gly Ser Asn Asn
 425 430 435
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 Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala Leu Ile Gly Gly
 440 445 450
 ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa aac gtc ccc gca 1507
 Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu Asn Val Pro Ala
 455 460 465
 gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac gcc tca gca atg 1555
 Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr Ala Ser Ala Met
 470 475 480 485
 tcc gat ttc tcc ggt gca tcc aac ctc act cca cac ctt gtt gaa tca 1603
 Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His Leu Val Glu Ser
 490 495 500
 ctt cca caa gca ctc cgt gaa gca att caa ctt tct tac aac gac gcc 1651
 Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser Tyr Asn Asp Ala
 505 510 515
 ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca gta gtc gcc gcg 1699
 Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala Val Val Ala Ala
 520 525 530
 atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag gaa acg cac gaa 1747
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 535 540 545
 taatgacaca cgaaacttcc gtc 1770

<210> 248

<211> 549

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 248

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 Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
 35 40 45
 Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
 50 55 60

Gln Thr Ile Ph Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65 70 75 80

Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
 85 90 95

Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
 100 105 110

Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
 115 120 125

Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
 130 135 140

Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
 145 150 155 160

Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
 165 170 175

Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
 180 185 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
 195 200 205

Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
 210 215 220

Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
 225 230 235 240

Ile Phe Met Ala Ile Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp
 245 250 255

Gly Gly Asn Glu Tyr Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe
 260 265 270

Ile Thr Thr Leu Val Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg
 275 280 285

Ala Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe
 290 295 300

Val Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly
 305 310 315 320

Thr Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn
 325 330 335

Pro Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile
 340 345 350

Gly Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr
 355 360 365

Lys Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val
 370 375 380
 Leu Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu
 385 390 395 400
 Tyr Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu
 405 410 415
 Val Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala
 420 425 430
 Thr Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser
 435 440 445
 Ala Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr
 450 455 460
 Glu Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln
 465 470 475 480
 Tyr Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro
 485 490 495
 His Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu
 500 505 510
 Ser Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile
 515 520 525
 Ala Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu
 530 535 540
 Lys Glu Thr His Glu
 545

<210> 249
 <211> 841
 <212> DNA
 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (101)..(841)
 <223> FRXA01314

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 Met Thr Ser Gln Val
 1 5
 aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca 163
 Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala
 10 15 20

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Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu	
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gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc	259
Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala	
40 45 50	
ctc atg ttg gcg atg ctt ctt agc tcc ttg ggt cag acc att ttc ggt	307
Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly Gln Thr Ile Phe Gly	
55 60 65	
tct gcc ctg cca acg att gtt ggt gag ctt ggc ggc gtt aac cac atg	355
Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met	
70 75 80 85	
acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct	403
Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro	
90 95 100	
att ttc ggc aag ttg ggt gac cag ttt ggt cgc aaa tac ctc ttc atg	451
Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met	
105 110 115	
ttt gcc atc gca ctg ttc gtg gtg ggt tcc atc atc ggt gct ttg gct	499
Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala	
120 125 130	
cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc	547
Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala	
135 140 145	
ggt ggt ggc ttg atg att ctt tct cag gca att acc gct gat gtc acc	595
Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr	
150 155 160 165	
acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc	643
Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe	
170 175 180	
gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac	691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp	
185 190 195	
ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc	739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile	
200 205 210	
atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa	787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu	
215 220 225	
cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc	835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile	
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gcc acc
Ala Thr

841

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<213> *Corynebacterium glutamicum*

<400> 250

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Ser Lys Ser Gly Ala Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala
      20           25           30

Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
      35           40           45

Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
      50           55           60

Gln Thr Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
      65           70           75           80

Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
      85           90           95

Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
      100          105          110

Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
      115          120          125

Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
      130          135          140

Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
      145          150          155          160

Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
      165          170          175

Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
      180          185          190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
      195          200          205

Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
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Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
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Ile Phe Met Ala Ile Ala Thr

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245

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 Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr
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 atc gcg tac atg cct acc tac ctg cag atg gtt cat ggt ctg aac cca 144
 Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro
 35 40 45
 acg caa gct ggt ctg atg ctg atc cca atg atg atc ggc ctg att ggt 192
 Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
 50 55 60
 aca tcc act gtg gtg ggc aac atc gtg tcc aag act ggc aag tac aag 240
 Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
 65 70 75 80
 tgg tac cca ttc atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg 288
 Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
 85 90 95
 cta tcg acg ctg aca cct tcg gca agc ttg gct ctc att gga ctg tac 336
 Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
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 ttc ttc gtc ttc gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt 384
 Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
 115 120 125
 ctc atc gtg cag aac tcc ttc cca atc acc atg gtt ggc acc gcg acc 432
 Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr
 130 135 140
 ggt tcc aac aac ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca 480
 Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala
 145 150 155 160
 ctg atc ggt ggc ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa 528
 Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu
 165 170 175

aac gtc ccc gca gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac 576
 Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
 180 185 190

gcc tca gca atg tcc gat ttc tcc ggt gca tcc aac ctc act cca cac 624
 Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
 195 200 205

ctt gtt gaa tca ctt cca caa gca ctc cgt gaa gca att caa ctt tct 672
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 210 215 220

tac aac gac gcc ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca 720
 Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
 225 230 235 240

gta gtc gcc gcg atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag 768
 Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys
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<213> Corynebacterium glutamicum

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Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro
 35 40 45

Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
 50 55 60

Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
 65 70 75 80

Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
 85 90 95

Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
 100 105 110

Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
 115 120 125

Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr

atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307

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Thr	Ile	Val	Gly	Glu	Leu	Gly	Gly	Val	Asp	His	Met	Met	Trp	Val	Ile	
70					75					80					85	
acc	gca	tac	cta	ctt	gcc	gaa	acc	atc	atg	ctg	ccg	atc	tac	gga	aag	403
Thr	Ala	Tyr	Leu	Leu	Ala	Glu	Thr	Ile	Met	Leu	Pro	Ile	Tyr	Gly	Lys	
				90					95					100		
ctc	ggc	gac	ctg	ggt	gga	cgt	aaa	ggt	ctc	ttc	atc	gga	gcc	ctc	ggc	451
Leu	Gly	Asp	Leu	Val	Gly	Arg	Lys	Gly	Leu	Phe	Ile	Gly	Ala	Leu	Gly	
			105					110					115			
atc	ttc	ctg	atc	ggc	tcc	gtc	atc	ggc	ggg	ctt	gca	gga	aat	atg	acc	499
Ile	Phe	Leu	Ile	Gly	Ser	Val	Ile	Gly	Gly	Leu	Ala	Gly	Asn	Met	Thr	
		120					125					130				
tgg	ttg	atc	gtc	ggc	cgt	gcc	gta	cag	ggc	atc	ggt	ggc	ggt	gga	ctg	547
Trp	Leu	Ile	Val	Gly	Arg	Ala	Val	Gln	Gly	Ile	Gly	Gly	Gly	Gly	Leu	
	135					140					145					
atg	atc	ctc	tgc	cag	gca	atc	atc	gcg	gac	ggt	ggt	cca	gca	cgt	gaa	595
Met	Ile	Leu	Ser	Gln	Ala	Ile	Ile	Ala	Asp	Val	Val	Pro	Ala	Arg	Glu	
150					155				160						165	
cgt	ggc	cgc	tac	atg	ggt	gtc	atg	ggt	gga	gtc	ttc	gga	ctc	tct	gca	643
Arg	Gly	Arg	Tyr	Met	Gly	Val	Met	Gly	Gly	Val	Phe	Gly	Leu	Ser	Ala	
				170				175						180		
ggt	ctt	ggc	cca	cta	ctc	ggt	ggc	tgg	ttc	acc	gaa	gga	cca	ggc	tgg	691
Val	Leu	Gly	Pro	Leu	Leu	Gly	Gly	Trp	Phe	Thr	Glu	Gly	Pro	Gly	Trp	
			185					190					195			
cgc	tgg	gca	ttc	tgg	atg	aac	atc	cca	ctg	gga	atc	atc	gcc	atc	ggt	739
Arg	Trp	Ala	Phe	Trp	Met	Asn	Ile	Pro	Leu	Gly	Ile	Ile	Ala	Ile	Gly	
		200					205					210				
gtc	gcc	att	tac	ttc	ctg	gac	att	cca	aag	aag	agc	gtc	aag	ttc	cgc	787
Val	Ala	Ile	Tyr	Phe	Leu	Asp	Ile	Pro	Lys	Lys	Ser	Val	Lys	Phe	Arg	
	215					220					225					
tgg	gat	tac	ctg	ggc	act	ttc	ttc	atg	atc	ggt	gcc	gca	acc	agc	ctg	835
Trp	Asp	Tyr	Leu	Gly	Thr	Phe	Phe	Met	Ile	Val	Ala	Ala	Thr	Ser	Leu	
230					235					240					245	
atc	ctg	ttc	acc	acc	tgg	ggt	gga	tcc	cag	tac	gag	tgg	tct	gat	cca	883
Ile	Leu	Phe	Thr	Thr	Trp	Gly	Gly	Ser	Gln	Tyr	Glu	Trp	Ser	Asp	Pro	
			250					255						260		
atc	atc	att	gga	ctg	atc	atc	acc	acc	atc	ggt	gcc	gct	gca	ctg	ctg	931
Il	Ile	Ile	Gly	Leu	Ile	Ile	Thr	Thr	Ile	Val	Ala	Ala	Ala	Leu	Leu	
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ggt	ggt	gtg	gaa	ctg	cgc	gca	aaa	gat	cca	ttg	ggt	cca	atg	tcc	ttc	979
Val	Val	Val	Glu	Leu	Arg	Ala	Lys	Asp	Pro	Leu	Val	Pro	Met	Ser	Phe	

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Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile Ala Gly Leu Ile Leu			
295	300	305	
ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag			1075
Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln			
310	315	320	325
atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca			1123
Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro			
330	335	340	
atg atg gtc ggc atg atg ggt acc tcc atc tgg act ggt atc cgc atc			1171
Met Met Val Gly Met Met Gly Thr Ser Ile Trp Thr Gly Ile Arg Ile			
345	350	355	
tcc aac aca gga aag tac aaa ctc ttc cca cca atc ggc atg gtg gtt			1219
Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val			
360	365	370	
acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc			1267
Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr			
375	380	385	
ctg tgg cag atc gga atc tac ctc ttc gtc ctc ggc gtc ggc ctg ggt			1315
Leu Trp Gln Ile Gly Ile Tyr Leu Phe Val Leu Gly Val Gly Leu Gly			
390	395	400	405
cta gcc atg cag gtt ctg gtc ctg atc gtt cag aac acc ctg cca acc			1363
Leu Ala Met Gln Val Leu Val Leu Ile Val Gln Asn Thr Leu Pro Thr			
410	415	420	
gcg gtg gtc gga tcc gca acc gct gtg aac aac ttc ttc cgt caa atc			1411
Ala Val Val Gly Ser Ala Thr Ala Val Asn Asn Phe Phe Arg Gln Ile			
425	430	435	
ggt tcc tca ctc gga tcc gcg ctg gtc ggt ggc atg ttc gtt ggc aac			1459
Gly Ser Ser Leu Gly Ser Ala Leu Val Gly Gly Met Phe Val Gly Asn			
440	445	450	
ttg gga acc ctc atg gaa gaa aga atg cca gca gcc atg gca caa ctt			1507
Leu Gly Thr Leu Met Glu Glu Arg Met Pro Ala Ala Met Ala Gln Leu			
455	460	465	
tca cca gaa gaa caa gcc gcc atg gca gcc caa ggc gga ctg gac tcc			1555
Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln Gly Gly Leu Asp Ser			
470	475	480	485
aac gaa ttg acg ccg gca atc gtc aat caa ttg cca acc gcg ctc cac			1603
Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu Pro Thr Ala Leu His			
490	495	500	
gat gcg ttc gcc ggt tcc tac aac gac gca ctc atc cca gtg ttc tac			1651
Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu Ile Pro Val Phe Tyr			
505	510	515	

gtg atg atg cca ctg atc ggc atc gcg ctg ctt ctc ttg ctg ttt att 1699
 Val Met Met Pro Leu Ile Gly Ile Ala Leu Leu Leu Leu Leu Phe Ile
 520 525 530

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cct 1755

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<213> Corynebacterium glutamicum

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Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser
 35 40 45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
 50 55 60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65 70 75 80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
 85 90 95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
 100 105 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
 115 120 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
 130 135 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
 145 150 155 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
 165 170 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
 195 200 205

Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
 210 215 220
 Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
 225 230 235 240
 Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
 245 250 255
 Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
 260 265 270
 Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
 275 280 285
 Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
 290 295 300
 Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
 305 310 315 320
 Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
 325 330 335
 Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
 340 345 350
 Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
 355 360 365
 Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
 370 375 380
 Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe Val Leu
 385 390 395 400
 Gly Val Gly Leu Gly Leu Ala Met Gln Val Leu Val Leu Ile Val Gln
 405 410 415
 Asn Thr Leu Pro Thr Ala Val Val Gly Ser Ala Thr Ala Val Asn Asn
 420 425 430
 Phe Phe Arg Gln Ile Gly Ser Ser Leu Gly Ser Ala Leu Val Gly Gly
 435 440 445
 Met Phe Val Gly Asn Leu Gly Thr Leu Met Glu Glu Arg Met Pro Ala
 450 455 460
 Ala Met Ala Gln Leu Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln
 465 470 475 480
 Gly Gly Leu Asp Ser Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu
 485 490 495
 Pro Thr Ala Leu His Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu
 500 505 510

Ile Pro Val Phe Tyr Val Met Met Pro Leu Ile Gly Ile Ala Leu L u
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 530 535 540

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 <223> FRXA01319

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 Met Thr His Glu Thr
 1 5
 tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg 163
 Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
 10 15 20
 cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct 211
 Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
 25 30 35
 gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc 259
 Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
 40 45 50
 atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307
 Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
 55 60 65
 aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc 355
 Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile
 70 75 80 85
 acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag 403
 Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys
 90 95 100
 ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc 451
 Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly
 105 110 115
 atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc 499
 Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr

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atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Ala Leu Leu 265 270 275			931
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ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln 310 315 320 325			1075
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 Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val
 360 365 370

acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc 1267
 Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr
 375 380 385

ctg tgg cag atc gga atc tac ctc ttc 1294
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<213> Corynebacterium glutamicum

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Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser
 35 40 45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
 50 55 60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65 70 75 80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
 85 90 95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
 100 105 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
 115 120 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
 130 135 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
 145 150 155 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
 165 170 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly

195 200 205
 Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
 210 215 220
 Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
 225 230 235 240
 Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
 245 250 255
 Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
 260 265 270
 Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
 275 280 285
 Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
 290 295 300
 Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
 305 310 315 320
 Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
 325 330 335
 Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
 340 345 350
 Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
 355 360 365
 Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
 370 375 380
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 385 390 395

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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (93)..(1487)
 <223> RXA01578

<400> 257
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 Met Ile Ala Leu Leu Val Ala
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 gta ttc gcc ttc cag ctc aac gcc tcc atg ctg gcg ccg gca ctg gcc 161

Val	Phe	Ala	Phe	Gln	Leu	Asn	Ala	Ser	Met	Leu	Ala	Pro	Ala	Leu	Ala		
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acc	atg	gaa	act	gaa	ctt	aat	gca	aca	gct	gcc	caa	atc	ggc	atg	acg	209	
Thr	Met	Glu	Thr	Glu	Leu	Asn	Ala	Thr	Ala	Ala	Gln	Ile	Gly	Met	Thr		
	25					30					35						
cag	act	gct	ttc	ttc	acc	gcg	gcg	gcg	ctg	ttt	tcc	ctg	ttc	ctg	cca	257	
Gln	Thr	Ala	Phe	Phe	Thr	Ala	Ala	Ala	Leu	Phe	Ser	Leu	Phe	Leu	Pro		
	40				45				50						55		
cgt	tgg	ggc	gat	ctg	att	ggg	cgc	cgc	aaa	gtg	ctg	gtc	ggc	atg	atg	305	
Arg	Trp	Gly	Asp	Leu	Ile	Gly	Arg	Arg	Lys	Val	Leu	Val	Gly	Met	Met		
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att	gtc	acc	ggg	att	gga	tgt	gtt	gtc	gct	gcc	ttt	gct	ccg	aat	gtg	353	
Ile	Val	Thr	Gly	Ile	Gly	Cys	Val	Val	Ala	Ala	Phe	Ala	Pro	Asn	Val		
			75					80						85			
acc	atc	ctc	ttc	ctg	ggc	cgc	ctg	att	caa	ggg	gtt	gct	ggc	cca	acc	401	
Thr	Ile	Leu	Phe	Leu	Gly	Arg	Leu	Ile	Gln	Gly	Val	Ala	Gly	Pro	Thr		
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gtg	cca	ctg	tgt	ctg	atc	att	ctg	cgc	cag	cag	gta	acc	aat	gaa	aag	449	
Val	Pro	Leu	Cys	Leu	Ile	Ile	Leu	Arg	Gln	Gln	Val	Thr	Asn	Glu	Lys		
	105					110					115						
caa	tat	gcg	cta	ctt	ctc	gga	att	gtt	acc	tct	gtc	aac	ggg	ggg	atc	497	
Gln	Tyr	Ala	Leu	Leu	Leu	Gly	Ile	Val	Thr	Ser	Val	Asn	Gly	Gly	Ile		
	120				125				130						135		
ggc	ggc	gtg	gac	gcg	ctt	gct	ggg	ggc	tgg	ttg	gct	gaa	aca	ctt	ggg	545	
Gly	Gly	Val	Asp	Ala	Leu	Ala	Gly	Gly	Trp	Leu	Ala	Glu	Thr	Leu	Gly		
			140					145						150			
ttc	cgt	tcc	atc	ttc	tgg	gtc	atg	gct	gct	ttc	tgc	gct	gtc	gct	gcc	593	
Phe	Arg	Ser	Ile	Phe	Trp	Val	Met	Ala	Ala	Phe	Cys	Ala	Val	Ala	Ala		
			155					160					165				
ctc	gca	ctg	ccg	ttc	agc	gtg	aag	gaa	tcc	acc	gct	gaa	gaa	acc	ccg	641	
Leu	Ala	Leu	Pro	Phe	Ser	Val	Lys	Glu	Ser	Thr	Ala	Glu	Glu	Thr	Pro		
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aag	atg	gac	tgg	ctt	ggg	gtg	ctg	cca	ctg	gcg	gtg	tcc	att	gga	tct	689	
Lys	Met	Asp	Trp	Leu	Gly	Val	Leu	Pro	Leu	Ala	Val	Ser	Ile	Gly	Ser		
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ttg	ctc	atg	gct	ttc	aac	gag	gcc	ggc	aaa	ctc	ggg	gcc	gcg	aac	tgg	737	
Leu	Leu	Met	Ala	Phe	Asn	Glu	Ala	Gly	Lys	Leu	Gly	Ala	Ala	Asn	Trp		
	200				205					210				215			
att	ctg	gtg	gtt	gtg	ctg	ttc	atc	atc	ggg	atc	gcc	gga	gtc	atc	ttc	785	
Ile	Leu	Val	Val	Val	Leu	Phe	Ile	Ile	Gly	Ile	Ala	Gly	Val	Ile	Phe		
			220						225					230			
ttc	tac	aac	att	gaa	aag	cgc	gtt	aag	cac	ccg	ctg	gtc	agt	gtt	gaa	833	
Phe	Tyr	Asn	Ile	Glu	Lys	Arg	Val	Lys	His	Pro	Leu	Val	Ser	Val	Glu		

235	240	245	
tac ctc ggt caa cga cgc acc tgg gca ttg ctg ctg agc acc ctt ctc Tyr Leu Gly Gln Arg Arg Thr Trp Ala Leu Leu Leu Ser Thr Leu Leu 250 255 260			881
aca atg acc ggt gta ttc gcc gta atg aat ggt ctg ctg ccc aac ctt Thr Met Thr Gly Val Phe Ala Val Met Asn Gly Leu Leu Pro Asn Leu 265 270 275			929
gcg cag gat gct gcc aac ggt gcc ggc atg tca gcg agc gtg gtg tcc Ala Gln Asp Ala Ala Asn Gly Ala Gly Met Ser Ala Ser Val Val Ser 280 285 290 295			977
tgg tgg aca ctt acc cca tat gcg ctg gct ggc ttg gta ttc ggt cca Trp Trp Thr Leu Thr Pro Tyr Ala Leu Ala Gly Leu Val Phe Gly Pro 300 305 310			1025
atc gcc gga att ctc gcc gga aaa ttt gga tac aag atc gtc ctg caa Ile Ala Gly Ile Leu Ala Gly Lys Phe Gly Tyr Lys Ile Val Leu Gln 315 320 325			1073
att ggt atc gct gcc acc atc atc ggc gtt gcc gga gcc acc ttc tta Ile Gly Ile Ala Ala Thr Ile Ile Gly Val Ala Gly Ala Thr Phe Leu 330 335 340			1121
gtc gga agc acc tcg cat ctc gcg tac ctc ggc atc tcc atc ttc gtg Val Gly Ser Thr Ser His Leu Ala Tyr Leu Gly Ile Ser Ile Phe Val 345 350 355			1169
ggt att acc tat gca ggt att gcc aac atc atg ctc aac ggc ctg ggc Gly Ile Thr Tyr Ala Gly Ile Ala Asn Ile Met Leu Asn Gly Leu Gly 360 365 370 375			1217
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gca ggt gcc ttc aac cta ggt gca ggt att tcc ttc gcc atc ctc ttc Ala Gly Ala Phe Asn Leu Gly Ala Gly Ile Ser Phe Ala Ile Leu Phe 395 400 405			1313
gca gtt tcc acg gca ttc agt gac aac ggc gga gga tac gcc gca ggc Ala Val Ser Thr Ala Phe Ser Asp Asn Gly Gly Gly Tyr Ala Ala Gly 410 415 420			1361
atg tgg gct ggc gtg atc atc ttg gtc cta gcc ttc ctc tgc tcc ctg Met Trp Ala Gly Val Ile Ile Leu Val Leu Ala Phe Leu Cys Ser Leu 425 430 435			1409
ctg atc cca cgc cca gaa tca atc acc gat aca gtg gca gcc aaa gtc Leu Ile Pro Arg Pro Glu Ser Ile Thr Asp Thr Val Ala Ala Lys Val 440 445 450 455			1457
cag gct gaa gaa gcc gct caa gcc gcc agc taaatccaca aactgaacta Gln Ala Glu Glu Ala Ala Gln Ala Ala Ser 460 465			1507

agg

1510

<210> 258

<211> 465

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

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Ala Ala Gln Ile Gly Met Thr Gln Thr Ala Phe Phe Thr Ala Ala Ala
 35 40 45

Leu Phe Ser Leu Phe Leu Pro Arg Trp Gly Asp Leu Ile Gly Arg Arg
 50 55 60

Lys Val Leu Val Gly Met Met Ile Val Thr Gly Ile Gly Cys Val Val
 65 70 75 80

Ala Ala Phe Ala Pro Asn Val Thr Ile Leu Phe Leu Gly Arg Leu Ile
 85 90 95

Gln Gly Val Ala Gly Pro Thr Val Pro Leu Cys Leu Ile Ile Leu Arg
 100 105 110

Gln Gln Val Thr Asn Glu Lys Gln Tyr Ala Leu Leu Leu Gly Ile Val
 115 120 125

Thr Ser Val Asn Gly Gly Ile Gly Gly Val Asp Ala Leu Ala Gly Gly
 130 135 140

Trp Leu Ala Glu Thr Leu Gly Phe Arg Ser Ile Phe Trp Val Met Ala
 145 150 155 160

Ala Phe Cys Ala Val Ala Ala Leu Ala Leu Pro Phe Ser Val Lys Glu
 165 170 175

Ser Thr Ala Glu Glu Thr Pro Lys Met Asp Trp Leu Gly Val Leu Pro
 180 185 190

Leu Ala Val Ser Ile Gly Ser Leu Leu Met Ala Phe Asn Glu Ala Gly
 195 200 205

Lys Leu Gly Ala Ala Asn Trp Ile Leu Val Val Val Leu Phe Ile Ile
 210 215 220

Gly Ile Ala Gly Val Ile Phe Phe Tyr Asn Ile Glu Lys Arg Val Lys
 225 230 235 240

His Pro Leu Val Ser Val Glu Tyr Leu Gly Gln Arg Arg Thr Trp Ala
 245 250 255

Leu Leu Leu Ser Thr Leu Leu Thr Met Thr Gly Val Phe Ala Val Met
 260 265 270
 Asn Gly Leu Leu Pro Asn Leu Ala Gln Asp Ala Ala Asn Gly Ala Gly
 275 280 285
 Met Ser Ala Ser Val Val Ser Trp Trp Thr Leu Thr Pro Tyr Ala Leu
 290 295 300
 Ala Gly Leu Val Phe Gly Pro Ile Ala Gly Ile Leu Ala Gly Lys Phe
 305 310 315 320
 Gly Tyr Lys Ile Val Leu Gln Ile Gly Ile Ala Ala Thr Ile Ile Gly
 325 330 335
 Val Ala Gly Ala Thr Phe Leu Val Gly Ser Thr Ser His Leu Ala Tyr
 340 345 350
 Leu Gly Ile Ser Ile Phe Val Gly Ile Thr Tyr Ala Gly Ile Ala Asn
 355 360 365
 Ile Met Leu Asn Gly Leu Gly Ile Val Leu Ser Pro Ala Asn Asn Gln
 370 375 380
 Gly Tyr Leu Pro Gly Met Asn Ala Gly Ala Phe Asn Leu Gly Ala Gly
 385 390 395 400
 Ile Ser Phe Ala Ile Leu Phe Ala Val Ser Thr Ala Phe Ser Asp Asn
 405 410 415
 Gly Gly Gly Tyr Ala Ala Gly Met Trp Ala Gly Val Ile Ile Leu Val
 420 425 430
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 435 440 445
 Asp Thr Val Ala Ala Lys Val Gln Ala Glu Glu Ala Ala Gln Ala Ala
 450 455 460
 Ser
 465

<210> 259

<211> 1470

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1447)

<223> RXA02087

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				Met	Thr	Pro	Ile	Val								
				1				5								
gag	tcc	agg	gcg	tgg	aaa	gct	ctg	ggc	gct	tta	agt	gtt	ggg	ctg	ttt	163
Glu	Ser	Arg	Ala	Trp	Lys	Ala	Leu	Gly	Ala	Leu	Ser	Val	Gly	Leu	Phe	
			10					15						20		
ctc	aca	ctg	ctt	gac	caa	tcg	ttg	gtg	gct	gtc	gcg	ctg	cca	aag	att	211
Leu	Thr	Leu	Leu	Asp	Gln	Ser	Leu	Val	Ala	Val	Ala	Leu	Pro	Lys	Ile	
			25					30					35			
caa	gag	gat	ttg	ggc	gag	agc	ctg	aac	caa	gag	gtg	tgg	gtg	tca	gag	259
Gln	Glu	Asp	Leu	Gly	Ala	Ser	Leu	Asn	Gln	Ala	Val	Trp	Val	Ser	Ala	
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gtt	tat	ttg	ctc	act	ttt	gag	gtg	cca	ctg	ttg	att	act	ggg	cgc	ttg	307
Val	Tyr	Leu	Leu	Thr	Phe	Ala	Val	Pro	Leu	Leu	Ile	Thr	Gly	Arg	Leu	
	55					60					65					
ggc	gat	cgt	tat	gga	cag	cga	aat	att	tat	ctt	gcc	ggc	atg	gct	gtg	355
Gly	Asp	Arg	Tyr	Gly	Gln	Arg	Asn	Ile	Tyr	Leu	Ala	Gly	Met	Ala	Val	
	70				75					80					85	
ttt	acc	ctc	gag	gag	ttg	gcc	tgt	gta	ttt	gca	cca	agc	atc	gaa	tgg	403
Phe	Thr	Leu	Ala	Ala	Leu	Ala	Cys	Val	Phe	Ala	Pro	Ser	Ile	Glu	Trp	
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ttg	att	gct	gct	cgc	gag	gtg	cag	ggc	ctg	ggc	gga	tct	ctt	ctt	aat	451
Leu	Ile	Ala	Ala	Arg	Ala	Val	Gln	Gly	Leu	Gly	Gly	Ser	Leu	Leu	Asn	
			105					110					115			
ccg	cag	ccc	ctg	agc	atc	att	cac	aag	att	ttc	gag	cat	gat	cgt	agg	499
Pro	Gln	Pro	Leu	Ser	Ile	Ile	His	Lys	Ile	Phe	Ala	His	Asp	Arg	Arg	
		120					125					130				
gga	gcc	gcc	acc	ggg	gtg	tgg	agt	gct	gtt	gcc	tca	tca	gct	gga	ctt	547
Gly	Ala	Ala	Thr	Gly	Val	Trp	Ser	Ala	Val	Ala	Ser	Ser	Ala	Gly	Leu	
	135					140					145					
ttc	ggg	cca	gtt	atc	ggc	ggc	gtt	ctg	gtg	ggg	tgg	atc	agc	tgg	cgt	595
Phe	Gly	Pro	Val	Ile	Gly	Gly	Val	Leu	Val	Gly	Trp	Ile	Ser	Trp	Arg	
	150				155					160					165	
gct	gtg	ttc	ttg	gtt	tat	gtg	ccg	ctc	gga	ttg	atc	tcc	cta	ttt	atg	643
Ala	Val	Phe	Leu	Val	Tyr	Val	Pro	Leu	Gly	Leu	Ile	Ser	Leu	Phe	Met	
			170						175					180		
gtg	gag	cgt	tat	gtg	cct	aaa	ctt	ccc	acg	gga	acc	tcg	aag	atc	gat	691
Val	Ala	Arg	Tyr	Val	Pro	Lys	Leu	Pro	Thr	Gly	Thr	Ser	Lys	Ile	Asp	
			185					190					195			
tgg	ctc	tcg	ggc	gag	gtc	tca	ctt	gtt	gct	gta	ctt	ggc				

Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly Thr Leu Ile Trp Val	
215 220 225	
tcc ctt gcc gtt ggt att gct gca gct gtg ctc ttt ata tgg atg caa	835
Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu Phe Ile Trp Met Gln	
230 235 240 245	
aca aga tcc aag gcg cca ctg atg ccg ttg agg att ttc aag acg cgc	883
Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg Ile Phe Lys Thr Arg	
250 255 260	
aac ttc gcg atc ggt gca ttt tcg atc ttc agc ctg ggc ttt acg gtg	931
Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser Leu Gly Phe Thr Val	
265 270 275	
tat tcc gtt aat ttg ccc atc atg ttg tat ctg caa acg gct cag gga	979
Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu Gln Thr Ala Gln Gly	
280 285 290	
atg tcg tcg cag ttg gcc ggt ttg atg ttg gtt ccg atg ggc atc atc	1027
Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val Pro Met Gly Ile Ile	
295 300 305	
tct gtg gtg atg tca cca gta att gga cga ttg gtg gat cgc ctg gca	1075
Ser Val Val Met Ser Pro Val Ile Gly Arg Leu Val Asp Arg Leu Ala	
310 315 320 325	
cca gga atg atc tcc aag atc gga ttc ggc gcg ctg att ttc tcg atg	1123
Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala Leu Ile Phe Ser Met	
330 335 340	
gcg ttg atg gct gtc ttt atg atc gcc aac cta tcg ccg tgg tgg cta	1171
Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu Ser Pro Trp Trp Leu	
345 350 355	
ctc atc ccg att att ttg ttc ggt agc tcc aac gcg atg agt ttt gca	1219
Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn Ala Met Ser Phe Ala	
360 365 370	
ccg aac tct gtg att gct ctg cgt gat gtt ccg cag gat tta gtg ggc	1267
Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro Gln Asp Leu Val Gly	
375 380 385	
tct gct tct ggt ttt tac aac acc tca cgc cag gtg ggc gct gtt ttg	1315
Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln Val Gly Ala Val Leu	
390 395 400 405	
ggc gcc gct acc ttg ggc gct gtg atg caa ata gga gtg ggc acg gtg	1363
Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile Gly Val Gly Thr Val	
410 415 420	
tcc ttc ggt gtt gcc atg ggt gcg gca atc ctg gtg aca ctc gtg ccc	1411
Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu Val Thr Leu Val Pro	
425 430 435	
tta atc ttt ggg ttc cta gcg gta acc caa ttt aga tagttgctcc	1457
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440

445

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1470

<210> 260

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

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20 25 30Ala Leu Pro Lys Ile Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala
35 40 45Val Trp Val Ser Ala Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu
50 55 60Ile Thr Gly Arg Leu Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu
65 70 75 80Ala Gly Met Ala Val Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala
85 90 95Pro Ser Ile Glu Trp Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly
100 105 110Gly Ser Leu Leu Asn Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe
115 120 125Ala His Asp Arg Arg Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala
130 135 140Ser Ser Ala Gly Leu Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly
145 150 155 160Trp Ile Ser Trp Arg Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu
165 170 175Ile Ser Leu Phe Met Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly
180 185 190Thr Ser Lys Ile Asp Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val
195 200 205Leu Gly Val Val Leu Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly
210 215 220Thr Leu Ile Trp Val Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu
225 230 235 240

Phe Ile Trp Met Gln Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg

245								250				255			
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260								265				270			
Leu	Gly	Phe	Thr	Val	Tyr	Ser	Val	Asn	Leu	Pro	Ile	Met	Leu	Tyr	Leu
275								280				285			
Gln	Thr	Ala	Gln	Gly	Met	Ser	Ser	Gln	Leu	Ala	Gly	Leu	Met	Leu	Val
290								295				300			
Pro	Met	Gly	Ile	Ile	Ser	Val	Val	Met	Ser	Pro	Val	Ile	Gly	Arg	Leu
305								310				315			
Val	Asp	Arg	Leu	Ala	Pro	Gly	Met	Ile	Ser	Lys	Ile	Gly	Phe	Gly	Ala
325								330				335			
Leu	Ile	Phe	Ser	Met	Ala	Leu	Met	Ala	Val	Phe	Met	Ile	Ala	Asn	Leu
340								345				350			
Ser	Pro	Trp	Trp	Leu	Leu	Ile	Pro	Ile	Ile	Leu	Phe	Gly	Ser	Ser	Asn
355								360				365			
Ala	Met	Ser	Phe	Ala	Pro	Asn	Ser	Val	Ile	Ala	Leu	Arg	Asp	Val	Pro
370								375				380			
Gln	Asp	Leu	Val	Gly	Ser	Ala	Ser	Gly	Phe	Tyr	Asn	Thr	Ser	Arg	Gln
385								390				395			
Val	Gly	Ala	Val	Leu	Gly	Ala	Ala	Thr	Leu	Gly	Ala	Val	Met	Gln	Ile
405								410				415			
Gly	Val	Gly	Thr	Val	Ser	Phe	Gly	Val	Ala	Met	Gly	Ala	Ala	Ile	Leu
420								425				430			
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Arg

<210> 261

<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1315)

<223> RXA02088

<400> 261

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Met Leu Thr Gln Lys

	1	5	
ata gaa tta gag gct aaa cca aaa atc cca gag gag atc tgg gtg ctg			163
Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu Glu Ile Trp Val Leu			
	10	15	20
ggt gtg gct gcg ttt att att gcg ctg ggc tat ggc ctg att gcg ccg			211
Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr Gly Leu Ile Ala Pro			
	25	30	35
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Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val Ser Phe Ala Ala Ala			
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agt gcg gtg gtg tcc atc ttt gcg ggc gcc cgg ttg ttg ttt gcg ccg			307
Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg Leu Leu Phe Ala Pro			
	55	60	65
atg tcg ggg agt ttg atc gat aag atc ggt tcc cgt cgt gtg tat ctc			355
Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser Arg Arg Val Tyr Leu			
	70	75	80
act ggt tta ctc acc gtg gct atc acc acg ggg ctt gtt gcg ttg gcg			403
Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly Leu Val Ala Leu Ala			
	90	95	100
cag gaa tac tgg cag att ctg ctg ctt cgt ggc atc gca ggt att ggt			451
Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly Ile Ala Gly Ile Gly			
	105	110	115
tcc acc atg ttt acg gtc tct gcc atg ggc ctg atc gtg aag atg gcg			499
Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu Ile Val Lys Met Ala			
	120	125	130
ccg gtg gag atc cgc ggg ccg tgt tcg tcg gta tat gcc agt tcg ttc			547
Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val Tyr Ala Ser Ser Phe			
	135	140	145
ctg ttt ggc aat att att ggc ccg gtt gtg ggt gct gcg atg tcc ggt			595
Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly Ala Ala Met Ser Gly			
	150	155	160
ttg ggc atg ccg tgg ccg ttc gcg att tat ggt gct tcc gtt ggc tta			643
Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly Ala Ser Val Gly Leu			
	170	175	180
gct gca ctt gtt gtg tgg tgg ccg atg ccg aaa acc aac gat tca ctt			691
Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys Thr Asn Asp Ser Leu			
	185	190	195
cgg aag gct gat agc aat agt gtg ccg gcg ttg cgc ttt gct gag gca			739
Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu Arg Phe Ala Glu Ala			
	200	205	210
att aag gat tct gcc tac cgc tcg gcg ttg ttt agt gct ttt gcc aat			787
Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe Ser Ala Phe Ala Asn			
	215	220	225

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ggt tgg tcg aac ttt ggt gtg cgt gtg gcg gtt ctt cca ctg ttt gcc 835
Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val Leu Pro Leu Phe Ala
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gca gct gca ttt agc aat ggc gga gct att gcg ggt ttt gcc atg gct 883
Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala Gly Phe Ala Met Ala
250 255 260

gcg ttc gcc gct gga aat gct ttg tgt ctg caa ttc gcg ggc gat ctc 931
Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln Phe Ala Gly Asp Leu
265 270 275

tca gat cgc att ggc cgt aaa ccg atg att att tcc ggg ctg atc gtc 979
Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile Ser Gly Leu Ile Val
280 285 290

aat gca gtg ttc acg gca atg atc gga ttc ggc aca gaa gtg tgg atc 1027
Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly Thr Glu Val Trp Ile
295 300 305

ctg atc acg gta tct gcg ttg gca ggt gct ggt gcg ggc ttg ctt aat 1075
Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly Ala Gly Leu Leu Asn
310 315 320 325

cca agt cag cag gcg gtg ctc gct gat gtt ata gat tcc cgc ccc ggc 1123
Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile Asp Ser Arg Pro Gly
330 335 340

gga aaa gtc tta gcg aat ttc caa atg gcg cag gat ttc ggt gcg att 1171
Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln Asp Phe Gly Ala Ile
345 350 355

gtt ggc ccg att ctc gta ggc atg atc gca gaa cag gca ggc ttc caa 1219
Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu Gln Ala Gly Phe Gln
360 365 370

atc gga ttc atg ctg tgt ggt gtg atc agt ttg ctg gct gcg gtc gca 1267
Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu Leu Ala Ala Val Ala
375 380 385

tgg atc ttc ggc cgg gag acg ctg cca acg gcg aaa gtc gag cag gta 1315
Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala Lys Val Glu Gln Val
390 395 400 405

taa atg acg caa ttg tgg gtc
1338

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<210> 262

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

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Met Leu Thr Gln Lys Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu
1 5 10 15

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Glu Ile Trp Val Leu Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr
 20 25 30

Gly Leu Ile Ala Pro Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val
 35 40 45

Ser Phe Ala Ala Ala Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg
 50 55 60

Leu Leu Phe Ala Pro Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser
 65 70 75 80

Arg Arg Val Tyr Leu Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly
 85 90 95

Leu Val Ala Leu Ala Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly
 100 105 110

Ile Ala Gly Ile Gly Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu
 115 120 125

Ile Val Lys Met Ala Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val
 130 135 140

Tyr Ala Ser Ser Phe Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly
 145 150 155 160

Ala Ala Met Ser Gly Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly
 165 170 175

Ala Ser Val Gly Leu Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys
 180 185 190

Thr Asn Asp Ser Leu Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu
 195 200 205

Arg Phe Ala Glu Ala Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe
 210 215 220

Ser Ala Phe Ala Asn Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val
 225 230 235 240

Leu Pro Leu Phe Ala Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala
 245 250 255

Gly Phe Ala Met Ala Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln
 260 265 270

Phe Ala Gly Asp Leu Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile
 275 280 285

Ser Gly Leu Ile Val Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly
 290 295 300

Thr Glu Val Trp Ile Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly
 305 310 315 320

Ala Gly Leu Leu Asn Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile
 325 330 335

Asp Ser Arg Pro Gly Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln
 340 345 350

Asp Phe Gly Ala Ile Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu
 355 360 365

Gln Ala Gly Phe Gln Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu
 370 375 380

Leu Ala Ala Val Ala Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala
 385 390 395 400

Lys Val Glu Gln Val
 405

<210> 263
 <211> 1239
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1216)
 <223> RXA00764

<400> 263
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acctgggacg actggattat taggggtgga attttcgctc atg aca ctc aag act 115
 Met Thr Leu Lys Thr
 1 5

agc gtt ttg gca cta ctc tta gat aac gtg cat gtt ctt ctg att gcg 163
 Ser Val Leu Ala Leu Leu Leu Asp Asn Val His Val Leu Leu Ile Ala
 10 15 20

aat cct gag tcg acc acg cag acg cag aaa ctt ttc cgt cgt gtg gtg 211
 Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu Phe Arg Arg Val Val
 25 30 35

cct gcg ttg atg gcg ctt gat ggt gtg tcg ctt gaa gcg agg ttt acg 259
 Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu Glu Ala Arg Phe Thr
 40 45 50

cac tat gga ggc cat gcg gag gaa atg gtt gcg ggt ttg acg gtg gat 307
 His Tyr Gly Gly His Ala Glu Glu Met Val Ala Gly Leu Thr Val Asp
 55 60 65

gat ttt gat gtg att atc ccc gcg ggt ggg gac ggc acc gtc aac gaa 355
 Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp Gly Thr Val Asn Glu
 70 75 80 85

gtg ata aat ggg tta ctt ggg tcg gcg gaa ggt gat ttt aga aac ctt 403

Val	Ile	Asn	Gly	Leu	Leu	Gly	Ser	Ala	Glu	Gly	Asp	Phe	Arg	Asn	Leu			
				90					95					100				
gag	gat	ttg	ccg	gcg	att	gcg	gtg	ttg	cca	acg	ggg	tct	gcc	aat	gtg	451		
Glu	Asp	Leu	Pro	Ala	Ile	Ala	Val	Leu	Pro	Thr	Gly	Ser	Ala	Asn	Val			
				105					110					115				
ttt	gcc	cgt	gcg	ctt	ggg	tac	ccc	act	gac	ccg	tat	gct	gcc	gct	gat	499		
Phe	Ala	Arg	Ala	Leu	Gly	Tyr	Pro	Thr	Asp	Pro	Tyr	Ala	Ala	Ala	Asp			
				120					125					130				
gcc	ctg	gtg	gag	ttg	att	cgg	aag	aac	cac	acc	aga	act	atc	acc	ttg	547		
Ala	Leu	Val	Glu	Leu	Ile	Arg	Lys	Asn	His	Thr	Arg	Thr	Ile	Thr	Leu			
				135					140					145				
ggg	acg	tgg	aag	ggg	gat	gat	cag	ggg	act	cgt	tgg	ttc	gcg	ggt	aat	595		
Gly	Thr	Trp	Lys	Gly	Asp	Asp	Gln	Gly	Thr	Arg	Trp	Phe	Ala	Val	Asn			
				150					155					160				
gct	ggg	ttt	ggg	att	gat	gcg	gat	gtt	att	gcc	agg	gtc	gaa	cgg	gcg	643		
Ala	Gly	Phe	Gly	Ile	Asp	Ala	Asp	Val	Ile	Ala	Arg	Val	Glu	Arg	Ala			
				170					175					180				
aga	tct	ttc	ggc	ttt	gcg	gct	tca	ccg	ttg	ttg	tat	ctg	cag	gtg	agt	691		
Arg	Ser	Phe	Gly	Phe	Ala	Ala	Ser	Pro	Leu	Leu	Tyr	Leu	Gln	Val	Ser			
				185					190					195				
ctt	cgg	gcg	tgg	gtg	aaa	act	cag	att	aag	cca	ccg	aaa	att	acc	gtg	739		
Leu	Arg	Ala	Trp	Val	Lys	Thr	Gln	Ile	Lys	Pro	Pro	Lys	Ile	Thr	Val			
				200					205					210				
gag	gcg	gtg	gac	agc	aaa	ggg	cac	aaa	ttg	caa	aaa	gag	gaa	gtg	cca	787		
Glu	Ala	Val	Asp	Ser	Lys	Gly	His	Lys	Leu	Gln	Lys	Glu	Glu	Val	Pro			
				215					220					225				
atg	ctg	ctt	gcc	tcg	aat	acc	aat	ccg	tgg	act	ttt	ttg	ggt	ccg	ctt	835		
Met	Leu	Leu	Ala	Ser	Asn	Thr	Asn	Pro	Trp	Thr	Phe	Leu	Gly	Pro	Leu			
				230					235					240				
cct	gtg	gtg	aca	aat	ccg	cag	aat	tct	ttt	gac	aca	ggg	ctg	ggg	ctt	883		
Pro	Val	Val	Thr	Asn	Pro	Gln	Asn	Ser	Phe	Asp	Thr	Gly	Leu	Gly	Leu			
				250					255					260				
ttt	ggc	ttg	act	agt	gtg	cga	gga	ttc	ggg	gga	gtg	gca	gcg	atg	atg	931		
Phe	Gly	Leu	Thr	Ser	Val	Arg	Gly	Phe	Gly	Gly	Val	Ala	Ala	Met	Met			
				265					270					275				
cac	ctg	att	ggc	gtg	ggg	cat	ggg	cgg	aag	ttg	gag	aag	ttg	atc	gct	979		
His	Leu	Ile	Gly	Val	Gly	His	Gly	Arg	Lys	Leu	Glu	Lys	Leu	Ile	Ala			
				280					285					290				
aag	cgc	acc	att	gct	ttt	gat	gat	gcg	gag	aaa	gta	acg	ctc	acg	tgc	1027		
Lys	Arg	Thr	Ile	Ala	Phe	Asp	Asp	Ala	Glu	Lys	Val	Thr	Leu	Thr	Cys			
				295					300					305				
gac	agc	gat	cag	cgt	ttc	caa	gtt	gat	ggg	gag	tat	gaa	ggc	aaa	cca	1075		
Asp	Ser	Asp	Gln	Arg	Phe	Gln												

310	315	320	325	
aca aag gtg gtg ttg gaa tca atc act gat gcg gtg cga gtg tat gcg				1123
Thr Lys Val Val Leu Glu Ser Ile Thr Asp Ala Val Arg Val Tyr Ala				
	330	335	340	
ccg aag acg cat ccg aca ccg ccg atc atg aat tgg gct gtc cat ttg				1171
Pro Lys Thr His Pro Thr Pro Pro Ile Met Asn Trp Ala Val His Leu				
	345	350	355	
ttt aag cac gtc cgt gat ttc ctc cgg gtg cgc acg ttt ggc atc				1216
Phe Lys His Val Arg Asp Phe Leu Arg Val Arg Thr Phe Gly Ile				
	360	365	370	
taggattcat cggagttttc ttc				1239

<210> 264

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Thr Leu Lys Thr Ser Val Leu Ala Leu Leu Leu Asp Asn Val His				
1	5	10	15	
Val Leu Leu Ile Ala Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu				
	20	25	30	
Phe Arg Arg Val Val Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu				
	35	40	45	
Glu Ala Arg Phe Thr His Tyr Gly Gly His Ala Glu Glu Met Val Ala				
	50	55	60	
Gly Leu Thr Val Asp Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp				
	65	70	75	80
Gly Thr Val Asn Glu Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly				
	85	90	95	
Asp Phe Arg Asn Leu Glu Asp Leu Pro Ala Ile Ala Val Leu Pro Thr				
	100	105	110	
Gly Ser Ala Asn Val Phe Ala Arg Ala Leu Gly Tyr Pro Thr Asp Pro				
	115	120	125	
Tyr Ala Ala Ala Asp Ala Leu Val Glu Leu Ile Arg Lys Asn His Thr				
	130	135	140	
Arg Thr Ile Thr Leu Gly Thr Trp Lys Gly Asp Asp Gln Gly Thr Arg				
	145	150	155	160
Trp Phe Ala Val Asn Ala Gly Phe Gly Ile Asp Ala Asp Val Ile Ala				
	165	170	175	
Arg Val Glu Arg Ala Arg Ser Phe Gly Phe Ala Ala Ser Pro Leu Leu				

180	185	190
Tyr Leu Gln Val Ser Leu Arg Ala Trp Val Lys Thr Gln Ile Lys Pro		
195	200	205
Pro Lys Ile Thr Val Glu Ala Val Asp Ser Lys Gly His Lys Leu Gln		
210	215	220
Lys Glu Glu Val Pro Met Leu Leu Ala Ser Asn Thr Asn Pro Trp Thr		
225	230	235 240
Phe Leu Gly Pro Leu Pro Val Val Thr Asn Pro Gln Asn Ser Phe Asp		
245	250	255
Thr Gly Leu Gly Leu Phe Gly Leu Thr Ser Val Arg Gly Phe Gly Gly		
260	265	270
Val Ala Ala Met Met His Leu Ile Gly Val Gly His Gly Arg Lys Leu		
275	280	285
Glu Lys Leu Ile Ala Lys Arg Thr Ile Ala Phe Asp Asp Ala Glu Lys		
290	295	300
Val Thr Leu Thr Cys Asp Ser Asp Gln Arg Phe Gln Val Asp Gly Glu		
305	310	315 320
Tyr Glu Gly Lys Pro Thr Lys Val Val Leu Glu Ser Ile Thr Asp Ala		
325	330	335
Val Arg Val Tyr Ala Pro Lys Thr His Pro Thr Pro Pro Ile Met Asn		
340	345	350
Trp Ala Val His Leu Phe Lys His Val Arg Asp Phe Leu Arg Val Arg		
355	360	365
Thr Phe Gly Ile		
370		

<210> 265

<211> 271

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXN03125

<400> 265

tgacaccggc gcgacgtatg gcattactgg cgtcacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgacggtt ttg gtt cta gcg ttc	115
Leu Val Leu Ala Phe	
1 5	

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163

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<400> 267
atgatgatgt cctcagcaag tccaagcgcc aagccatgct ggaaacaatt ctcgagctga 60

taccaagcca gacttaaatt tctaccttaa agtcttgagc atg act gtt cag gaa 115
                                     Met Thr Val Gln Glu
                                     1                               5

ttc gac cgc gcg acc aaa ccc aca cca aaa ccc cca att gtt tct tgg 163
Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro Pro Ile Val Ser Trp
                               10                               15                               20

gcg ttt tqg gat tgg ggt tcc gcc tct ttc aac qcq qtc ctc qtq acc 211

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Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn Ala Val Leu Val Thr	
25 30 35	
ttt att ttc tcg gtc tat ctc act gat tca gtc ggc gcc acc ctc ccc	259
Phe Ile Phe Ser Val Tyr Leu Thr Asp Ser Val Gly Ala Thr Leu Pro	
40 45 50	
gag ggt tcc aac gcc aca tca ctg tat tcg atg gcg gtc gcc atc gct	307
Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met Ala Val Ala Ile Ala	
55 60 65	
ggc gtc att gtt gcg gtt gtt gcc cca gtc atg ggc agg cga tca gat	355
Gly Val Ile Val Ala Val Val Ala Pro Val Met Gly Arg Arg Ser Asp	
70 75 80 85	
atc aag ggc act cgc cgc agg tca ctg cgc atg tgg aca ctt gtc acc	403
Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met Trp Thr Leu Val Thr	
90 95 100	
gtg ttc ttg atg ttt tgt ctc ttt aca gta aag aac act gat ccc aca	451
Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys Asn Thr Asp Pro Thr	
105 110 115	
ttt ttc tgg ttt ggt gta gcc atc atg gcg atc gcc aac atc acc ttt	499
Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile Ala Asn Ile Thr Phe	
120 125 130	
gag ttc gct gaa gtt cag tac tat gcg cag ctc tcc caa atc tcg acc	547
Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu Ser Gln Ile Ser Thr	
135 140 145	
cgc gaa aac gtg ggc cga gtt tct ggt ttc ggc tgg tcc atg ggt tac	595
Arg Glu Asn Val Gly Arg Val Ser Gly Phe Gly Trp Ser Met Gly Tyr	
150 155 160 165	
ttc ggt ggc atc gtt cta ctg ctt gtt tgt tac cta ggt ttt gtt gcc	643
Phe Gly Gly Ile Val Leu Leu Leu Val Cys Tyr Leu Gly Phe Val Ala	
170 175 180	
ggt gat ggc gat acc cgc gga ttc cta aac ctg ccc atc gaa gac ggc	691
Gly Asp Gly Asp Thr Arg Gly Phe Leu Asn Leu Pro Ile Glu Asp Gly	
185 190 195	
atg aat atc cgc ctc gtc gca gtg ctt gca gcc gtt tgg ttc ttg gtc	739
Met Asn Ile Arg Leu Val Ala Val Leu Ala Ala Val Trp Phe Leu Val	
200 205 210	
tct gcg att ccg gca ctt ctt cga gtc cca gaa att gag gca cag gta	787
Ser Ala Ile Pro Ala Leu Leu Arg Val Pro Glu Ile Glu Ala Gln Val	
215 220 225	
gct gcc gaa gac cac ccc aaa ggc ctc ata gct gcc tac aag gat ctc	835
Ala Ala Glu Asp His Pro Lys Gly Leu Ile Ala Ala Tyr Lys Asp Leu	
230 235 240 245	
ttt ggg cag atc gct gag ctg tgg aaa caa gac cgc aac tcc gtg tat	883
Phe Gly Gln Ile Ala Glu Leu Trp Lys Gln Asp Arg Asn Ser Val Tyr	

250	255	260	
ttc ctc atc gca gca act gtt ttc cgt gac gga ctc gcc gga gta ttt			931
Phe Leu Ile Ala Ala Thr Val Phe Arg Asp Gly Leu Ala Gly Val Phe			
265	270	275	
acc ttc ggt gcc atc ctt gcg gtc tct gtg tac gga cta tct gcc ggt			979
Thr Phe Gly Ala Ile Leu Ala Val Ser Val Tyr Gly Leu Ser Ala Gly			
280	285	290	
gat gtc ctc ctc ttc ggt gtc gca gcc aac gtg gtc tct gcg ttg gga			1027
Asp Val Leu Leu Phe Gly Val Ala Ala Asn Val Val Ser Ala Leu Gly			
295	300	305	
gca ctc ctc gga gga ttc cta gac gat cgc gtc ggg cca aaa ccc atc			1075
Ala Leu Leu Gly Gly Phe Leu Asp Asp Arg Val Gly Pro Lys Pro Ile			
310	315	320	325
atc ttg att tct ctt gcc atc atg atc gcc gat gct gca att ctc ttc			1123
Ile Leu Ile Ser Leu Ala Ile Met Ile Ala Asp Ala Ala Ile Leu Phe			
330	335	340	
ttc gtt gaa ggc ccc act aat ttc tgg atc ttc gga tta atc ctc tgt			1171
Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe Gly Leu Ile Leu Cys			
345	350	355	
gcg ttt gtg gga cct gca cag tca gcg tcg aga agc tat tta aca cgt			1219
Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg Ser Tyr Leu Thr Arg			
360	365	370	
ctt tcc cca gat ggc cag gaa ggc cag ctc ttc ggc ctt tat gcc act			1267
Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe Gly Leu Tyr Ala Thr			
375	380	385	
acc ggc cgt gcc gtg agt tgg atg gtg ccg tcg ctg ttt ggt gta ttt			1315
Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser Leu Phe Gly Val Phe			
390	395	400	405
gtg ggg ctc acc ggc gat gac cgc act ggt att ttg gcc atc gcg ctg			1363
Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile Leu Ala Ile Ala Leu			
410	415	420	
att ctg cta ttc ggt att gtg ctg ctg agc atg gtg aag cca ccg cac			1411
Ile Leu Leu Phe Gly Ile Val Leu Leu Ser Met Val Lys Pro Pro His			
425	430	435	
aag gtg aag tagacaaagc gccacaagg att			1443
Lys Val Lys			
440			

<210> 268

<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Thr Val Gln Glu Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro
 1 5 10 15
 Pro Ile Val Ser Trp Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn
 20 25 30
 Ala Val Leu Val Thr Phe Ile Phe Ser Val Tyr Leu Thr Asp Ser Val
 35 40 45
 Gly Ala Thr Leu Pro Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met
 50 55 60
 Ala Val Ala Ile Ala Gly Val Ile Val Ala Val Val Ala Pro Val Met
 65 70 75 80
 Gly Arg Arg Ser Asp Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met
 85 90 95
 Trp Thr Leu Val Thr Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys
 100 105 110
 Asn Thr Asp Pro Thr Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile
 115 120 125
 Ala Asn Ile Thr Phe Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu
 130 135 140
 Ser Gln Ile Ser Thr Arg Glu Asn Val Gly Arg Val Ser Gly Phe Gly
 145 150 155 160
 Trp Ser Met Gly Tyr Phe Gly Gly Ile Val Leu Leu Leu Val Cys Tyr
 165 170 175
 Leu Gly Phe Val Ala Gly Asp Gly Asp Thr Arg Gly Phe Leu Asn Leu
 180 185 190
 Pro Ile Glu Asp Gly Met Asn Ile Arg Leu Val Ala Val Leu Ala Ala
 195 200 205
 Val Trp Phe Leu Val Ser Ala Ile Pro Ala Leu Leu Arg Val Pro Glu
 210 215 220
 Ile Glu Ala Gln Val Ala Ala Glu Asp His Pro Lys Gly Leu Ile Ala
 225 230 235 240
 Ala Tyr Lys Asp Leu Phe Gly Gln Ile Ala Glu Leu Trp Lys Gln Asp
 245 250 255
 Arg Asn Ser Val Tyr Phe Leu Ile Ala Ala Thr Val Phe Arg Asp Gly
 260 265 270
 Leu Ala Gly Val Phe Thr Phe Gly Ala Ile Leu Ala Val Ser Val Tyr
 275 280 285
 Gly Leu Ser Ala Gly Asp Val Leu Leu Phe Gly Val Ala Ala Asn Val
 290 295 300

Val Ser Ala Leu Gly Ala Leu Leu Gly Gly Phe Leu Asp Asp Arg Val
 305 310 315 320

Gly Pro Lys Pro Ile Ile Leu Ile Ser Leu Ala Ile Met Ile Ala Asp
 325 330 335

Ala Ala Ile Leu Phe Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe
 340 345 350

Gly Leu Ile Leu Cys Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg
 355 360 365

Ser Tyr Leu Thr Arg Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe
 370 375 380

Gly Leu Tyr Ala Thr Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser
 385 390 395 400

Leu Phe Gly Val Phe Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile
 405 410 415

Leu Ala Ile Ala Leu Ile Leu Leu Phe Gly Ile Val Leu Leu Ser Met
 420 425 430

Val Lys Pro Pro His Lys Val Lys
 435 440

<210> 269
 <211> 840
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(817)
 <223> RXN00535

<400> 269
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cctaaggagc tcacctttac tcaatgctct gatgacaccg atg tgg tgg gca ggc 115
 Met Trp Trp Ala Gly
 1 5

atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt 163
 Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
 10 15 20

ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tcg ctg atg 211
 Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
 25 30 35

ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga 259
 Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
 40 45 50

act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg	307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met	
55 60 65	
atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat	355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp	
70 75 80 85	
cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg	403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met	
90 95 100	
tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt	451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu	
105 110 115	
ggt ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa	499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys	
120 125 130	
gcc gcg gtg gat ctt ttt gtc cat caa ggc ata acg gga ctc atc ttg	547
Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu	
135 140 145	
aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc	595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile	
150 155 160 165	
gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc	643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro	
170 175 180	
gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg	691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu	
185 190 195	
gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg	739
Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met	
200 205 210	
ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt	787
Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg	
215 220 225	
aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc	837
Thr Ser Thr Met Pro Ala Gly Ser Lys Arg	
230 235	
cga	840

<210> 270

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

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 35 40 45
 Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
 50 55 60
 Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
 65 70 75 80
 His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
 85 90 95
 Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
 100 105 110
 Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
 115 120 125
 Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
 130 135 140
 Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
 145 150 155 160
 Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
 165 170 175
 Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
 180 185 190
 Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
 195 200 205
 Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr
 210 215 220
 Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
 225 230 235

<210> 271

<211> 2472

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2449)

<223> RXN00453

<400> 271

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attcaggttg gggcgatggt cctataatcg caagtggatt gtg att tcg gca tgg 115
Val Ile Ser Ala Trp
1 5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag 163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
10 15 20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc 211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
25 30 35

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg 259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
40 45 50

gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt 307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
55 60 65

gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att 355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
70 75 80 85

gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct 403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu Arg Phe Gly Asn Pro
90 95 100

gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc 451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr
105 110 115

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg 499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu
120 125 130

gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att 547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile
135 140 145

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc 595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile
150 155 160 165

aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc 643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala
170 175 180

ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag 691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu
185 190 195

atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt 739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly
200 205 210

tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr Ala Val Ile Gly Val 215 220 225	787
ggc att ggt gcg ctg gca att gtg ctg gcc acg gcg ttt act gat ctc Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr Ala Phe Thr Asp Leu 230 235 240 245	835
aac aat gtg act cca gtg ctc gca gtg atg att ggc ctg gcc gtg ggc Asn Asn Val Thr Pro Val Leu Ala Val Met Ile Gly Leu Ala Val Gly 250 255 260	883
att gac tac gcg ctg ttt att ttg tct agg tac cgt gcg gag tat aag Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr Arg Ala Glu Tyr Lys 265 270 275	931
cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala Val Gly Thr Ala Gly 280 285 290	979
agt gcg gtg gtg ttt gct ggc gcg acg gtg att atc gcg ctg gta gcc Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile Ile Ala Leu Val Ala 295 300 305	1027
ctc atc att gcg gat atc gga ttc ctc acg gcc atg ggt att tct gcg Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala Met Gly Ile Ser Ala 310 315 320 325	1075
gcg ttt acg gtg ttc gtg gct gtg ctc att gcg ttg acg ttt atc ccg Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro 330 335 340	1123
gcg ctg ttg ggt gtg ttt ggt ggt cat gcg ttc aag ggc aag atc cct Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro 345 350 355	1171
gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu 360 365 370	1219
aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys Leu Val Gln Lys Ala 375 380 385	1267
ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr 390 395 400 405	1315
att cct gca atg aac ctg cag ttg tca ctg cct tct gac tcc acc tcc Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro Ser Asp Ser Thr Ser 410 415 420	1363
aat att gat acc act cag cgt cag tcg gct gat ttg atg gca gag ggc Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly 425 430 435	1411

ttt ggc gcg ggc gtt aat gcg ccg ttc ttg gtc atc gtc gat acg cat	1459
Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His	
440 445 450	
gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag	1507
Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln	
455 460 465	
gag cct gaa gag ggc gag ttc gat cgg gag cag gcg gct cgt ttt gct	1555
Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala	
470 475 480 485	
acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag	1603
Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys	
490 495 500	
aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att	1651
Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe Thr Ala Ala Gln Ile	
505 510 515	
ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg	1699
Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu	
520 525 530	
atg cac gtg ctg cgt gcg cag gaa gct cag att gag gat gtt acg gga	1747
Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly	
535 540 545	
act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act	1795
Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr	
550 555 560 565	
gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt	1843
Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly	
570 575 580	
ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg	1891
Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro	
585 590 595	
ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt	1939
Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val Gly Ala Ala Phe Gly	
600 605 610	
gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc	1987
Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr	
615 620 625	
cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc ggc gtg acc	2035
Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr	
630 635 640 645	
ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc	2083
Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg	
650 655 660	
gag cac tac acc cac cac aat ggc aag gga cag cct ggt tcc aag tac	2131

Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr
 665 670 675
 acc ccg gtt gag cag tca gtg att gaa ggc ttc acg cag ggc tcc cgc 2179
 Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg
 680 685 690
 gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt 2227
 Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe
 695 700 705
 att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt 2275
 Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly
 710 715 720 725
 gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc 2323
 Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro
 730 735 740
 gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg 2371
 Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp
 745 750 755
 ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag 2419
 Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu
 760 765 770
 aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca 2469
 Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
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 gat 2472

<210> 272

<211> 783

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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 Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
 35 40 45
 Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
 50 55 60
 Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala
 65 70 75 80
 Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu
 85 90 95

Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val
 100 105 110
 Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys
 115 120 125
 Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr
 130 135 140
 Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys
 145 150 155 160
 His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly
 165 170 175
 Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile
 180 185 190
 Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu
 195 200 205
 Ile Phe Thr Phe Gly Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr
 210 215 220
 Ala Val Ile Gly Val Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr
 225 230 235 240
 Ala Phe Thr Asp Leu Asn Asn Val Thr Pro Val Leu Ala Val Met Ile
 245 250 255
 Gly Leu Ala Val Gly Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr
 260 265 270
 Arg Ala Glu Tyr Lys Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala
 275 280 285
 Val Gly Thr Ala Gly Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile
 290 295 300
 Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala
 305 310 315 320
 Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala
 325 330 335
 Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe
 340 345 350
 Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr
 355 360 365
 Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys
 370 375 380
 Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly
 385 390 395 400

Leu Gly Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro
 405 410 415
 Ser Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp
 420 425 430
 Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val
 435 440 445
 Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro
 450 455 460
 Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln
 465 470 475 480
 Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser
 485 490 495
 Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
 500 505 510
 Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
 515 520 525
 Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
 530 535 540
 Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
 545 550 555 560
 Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
 565 570 575
 Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
 580 585 590
 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
 595 600 605
 Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
 610 615 620
 Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
 625 630 635 640
 Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
 645 650 655
 Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
 660 665 670
 Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
 675 680 685
 Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
 690 695 700

Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
 705 710 715 720

Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
 725 730 735

Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
 740 745 750

Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu
 755 760 765

Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
 770 775 780

<210> 273
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> RXN00932

<400> 273
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aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa 115
 Met Thr Pro Gln Lys
 1 5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
 Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
 10 15 20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211
 Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
 25 30 35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259
 Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
 40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
 Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
 55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355
 Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
 70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403
 Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
 90 95 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451
 Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
 105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
 Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
 120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
 Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
 135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
 Pro Asp Ala Ile Ala Asn Thr Val Asp
 150 155

atg 597

<210> 274
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 274
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 20 25 30
 Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
 35 40 45
 Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
 50 55 60
 Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65 70 75 80
 Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
 85 90 95
 Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
 100 105 110
 Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
 115 120 125
 Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
 130 135 140
 Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
 145 150 155

<210> 275
 <211> 534
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (65)..(511)
 <223> RXN03022

<400> 275
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 agcagtg atc atc acc gct ggc atc ttg gta gcg acc gcg acc gcc ctc 109
 Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu
 1 5 10 15
 cta atg atc acc gcg gtc agc gag tca acg tac atc gtc atc tcc ctc 157
 Leu Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu
 20 25 30
 gcc ggc ttc tcc ctt tat ggc ctt ggc ctc gga ctc ttc gcc acc cca 205
 Ala Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro
 35 40 45
 gtc acc gat act gcg ctt gga aca ctt ccc aaa gac cgt acc ggc gct 253
 Val Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala
 50 55 60
 ggt gca ggt gta ttc aag atg tcc tct tcc ctc ggc gca gca ctc ggc 301
 Gly Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly
 65 70 75
 atc gca atc tcc act tca gtg ttc ctc gca ctt cgc gac ggc acc tcc 349
 Ile Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser
 80 85 90 95
 atc aac tcc gac gtc gca ctc gcc gga aca gtt tca ctt ggc atc aac 397
 Ile Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn
 100 105 110
 gtt gta ttc gca gca aca gcc acc atc acc gca gca gtc ctt att cca 445
 Val Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro
 115 120 125
 aaa gcc gct ggc aaa gtc tca caa acc agc atc acc ctt cct gag cca 493
 Lys Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro
 130 135 140
 gct atc gct gta aaa atc taaaacttca ccaggacaga taa 534
 Ala Ile Ala Val Lys Ile
 145

<210> 276
 <211> 149
 <212> PRT

<213> *Corynebacterium glutamicum*

<400> 276

Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu
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Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala
 20 25 30

Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val
 35 40 45

Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly
 50 55 60

Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile
 65 70 75 80

Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile
 85 90 95

Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val
 100 105 110

Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys
 115 120 125

Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala
 130 135 140

Ile Ala Val Lys Ile
 145

<210> 277

<211> 586

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(586)

<223> RXN03151

<400> 277

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agtatttggt taaccatcca cctcaaggag taaaacgcac gtg ctt tcc cac atc 115
 Val Leu Ser His Ile
 1 5

att gat gtc ctc gcc gac ccg atc gat ggc acc cca ctt gta ggc gcc 163
 Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr Pro Leu Val Gly Ala
 10 15 20

gaa gat ttc tca cgg ttg gtg tct gaa tct ggg cat tcc tac gat gtt 211
 Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly His Ser Tyr Asp Val

25	30	35	
gct cgt caa ggg tat gtc acc ctg gct ggt ggc gca ggt ctg cgc tat			259
Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly Ala Gly Leu Arg Tyr			
40	45	50	
tca ggc gat gat gca cag atg atc gcg gat cgg gaa acc ttc ctt tct			307
Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg Glu Thr Phe Leu Ser			
55	60	65	
ggc ggt cac ttc gcg ccc ttc gtg gaa gct gtc acc gag cat gtt caa			355
Gly Gly His Phe Ala Pro Phe Val Glu Ala Val Thr Glu His Val Gln			
70	75	80	85
gat gtc gtt gac cag gca ggc ctt agc gat gac gca cag cca gtg gtc			403
Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp Ala Gln Pro Val Val			
90	95	100	
tgc gaa atc ggc gcg gga acc ggc tac tac ttg tcc cat acc ctt gat			451
Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu Ser His Thr Leu Asp			
105	110	115	
tct gtt gca gga tct cgc gga att ggc att gac gtt tcc gtg cac gcc			499
Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp Val Ser Val His Ala			
120	125	130	
gca aag cgt ttg gca aag tgt cac cct cgc gtc ggc gca gtc atc gcg			547
Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val Gly Ala Val Ile Ala			
135	140	145	
aac gca tgg gca cgc ctg ccg att gca gat aac tcc tcg			586
Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn Ser Ser			
150	155	160	

<210> 278

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val	Leu	Ser	His	Ile	Ile	Asp	Val	Leu	Ala	Asp	Pro	Ile	Asp	Gly	Thr
1				5					10					15	

Pro	Leu	Val	Gly	Ala	Glu	Asp	Phe	Ser	Arg	Leu	Val	Ser	Glu	Ser	Gly
		20						25					30		

His	Ser	Tyr	Asp	Val	Ala	Arg	Gln	Gly	Tyr	Val	Thr	Leu	Ala	Gly	Gly
		35					40					45			

Ala	Gly	Leu	Arg	Tyr	Ser	Gly	Asp	Asp	Ala	Gln	Met	Ile	Ala	Asp	Arg
	50					55					60				

Glu	Thr	Phe	Leu	Ser	Gly	Gly	His	Phe	Ala	Pro	Phe	Val	Glu	Ala	Val
65					70				75					80	

Thr	Glu	His	Val	Gln	Asp	Val	Val	Asp	Gln	Ala	Gly	Leu	Ser	Asp	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Ala Gln Pro Val Val Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu
 100 105 110

Ser His Thr Leu Asp Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp
 115 120 125

Val Ser Val His Ala Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val
 130 135 140

Gly Ala Val Ile Ala Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn
 145 150 155 160

Ser Ser

<210> 279

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(543)

<223> RXN02832

<400> 279

cgc ggc cca gtg atg gat tat aca aat caa tca tta gta gca ttt ttc 48
 Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
 1 5 10 15

ttt aaa gca tta acg tca tat tta aag aaa cac aat tgt tta tat gtc 96
 Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
 20 25 30

ctt gta gat cca tat tta att gaa aat tta cgc aat gca gac ggt gaa 144
 Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
 35 40 45

att gtt aaa tct tat gat aac cga gca ttt gtt aga aca atg gat aaa 192
 Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
 50 55 60

tta ggt tat aaa cac caa ggt ttc cct gta ggt tat gat tca atg agc 240
 Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
 65 70 75 80

caa atc cgt tgg ctg tca gtg tta gat tta aaa gat aag act gaa gac 288
 Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
 85 90 95

caa ctt tta aaa gaa atg gat tat caa acg aga cgt aat att aaa aaa 336
 Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
 100 105 110

aca tat gat att ggt gtc aaa act aaa acg tta acg att gat gaa acg 384
 Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
 115 120 125

caa act ttt ttc gac tta ttc cat atg gct gag gaa aag cac ggt ttc 432
 Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
 130 135 140

aaa ttc cgt gag tta cca tac ttt gaa gaa atg caa aag tta tac gat 480
 Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
 145 150 155 160

gac cac gcc atg tta aag ttg gcg tat att gat tta aac gag tat tta 528
 Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
 165 170 175

aaa acg ttg caa tta 543
 Lys Thr Leu Gln Leu
 180

<210> 280
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
 Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
 1 5 10 15

Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
 20 25 30

Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
 35 40 45

Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
 50 55 60

Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
 65 70 75 80

Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
 85 90 95

Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
 100 105 110

Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
 115 120 125

Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
 130 135 140

Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
 145 150 155 160

Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
 165 170 175

Lys Thr Leu Gln Leu
 180

<210> 281
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> RXN00165

<400> 281
 aaacctcccc gggcccggcg cgcgaccgtc caagatgccg gcgttggatg ccaaattatg 60

gactctcaaa gtggcgttgt cgcagcggcc gtggagcttt gtg gcg tct gct ggc 115
 Val Ala Ser Ala Gly
 1 5

atg gcg gcg tct ttt atc tgc aat ggg tta acg cct gtg att gtg ggt 163
 Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr Pro Val Ile Val Gly
 10 15 20

aag gcg gtg gat gag gct att ggc acg agc gat ctg cag cga ttg tgg 211
 Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp Leu Gln Arg Leu Trp
 25 30 35

ttc tgg att gcc atg ttg gcg gtt ctt ttc tta acg gcg atg acg gtg 259
 Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu Thr Ala Met Thr Val
 40 45 50

aac tgg att gct cgg tac atg ttg gtg cgg agc cag cag ttg gtc agc 307
 Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser Gln Gln Leu Val Ser
 55 60 65

cat gat ttg cgc atg ttg gtg act gat cgg att caa gat ccg cgt ggt 355
 His Asp Leu Arg Met Leu Val Thr Asp Arg Ile Gln Asp Pro Arg Gly
 70 75 80 85

ttt gct gga aaa gag cgc act gcg ggt gga ttg ttg tcg att gcg tca 403
 Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu Leu Ser Ile Ala Ser
 90 95 100

tcg gat acg cag cgg gtg ggc gat atc gtc atg atg acg gtg ttc ccg 451
 Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met Met Thr Val Phe Pro
 105 110 115

gtg gcg gaa ttg gcg tcg att att tat ggc gcc gtg gtg atg tac agc 499
 Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala Val Val Met Tyr Ser
 120 125 130

att aat ccg tgg ttg agt gtg gct gtg ctg att ggt gga ccg ctg ctg 547

Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile Gly Gly Pro Leu Leu	
135 140 145	
gtt gtg gtg gct att cag gtc tca aag ccg ttg cag aag cgt tcg ggt	595
Val Val Val Ala Ile Gln Val Ser Lys Pro Leu Gln Lys Arg Ser Gly	
150 155 160 165	
gct cgt cag cag gcg gtg gca cag gct gcg gct act gca act gat gtg	643
Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala Thr Ala Thr Asp Val	
170 - 175 180	
gtg cag ggc ttg aga att ttg aag ggt ttg ggc gcg att gtc acg gtg	691
Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly Ala Ile Val Thr Val	
185 190 195	
cgc cgt cgg tac gag gcg att tct ggt gag gct tat cgg aag acg gtt	739
Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala Tyr Arg Lys Thr Val	
200 205 210	
cat gcg gat gct gcg gaa gct cgc ttg aat ggt gtc acc gat gcg gcg	787
His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly Val Thr Asp Ala Ala	
215 220 225	
ggc gcc atc ttt gtg tcc gcg ttg ggt att gga gca gga ttt ttg gcg	835
Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly Ala Gly Phe Leu Ala	
230 235 240 245	
ctg caa ggt cag atg agt att ggt gat ttg atc acg gtt gtg gga ctc	883
Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile Thr Val Val Gly Leu	
250 255 260	
aca cag ttt ttg atc atg ccg atg acc atg ctt ggt cga aat gtg gca	931
Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu Gly Arg Asn Val Ala	
265 270 275	
tcg cgc tgg gca tcg gcg gag gcg tcg gca aag cgt att agg gga gtg	979
Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys Arg Ile Arg Gly Val	
280 285 290	
ctc ggt gct gat ttt gag aga gtg tct gcg cat gat gcg gac aag gct	1027
Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His Asp Ala Asp Lys Ala	
295 300 305	
gag gag att atc caa caa ctt gcc aaa ggt ttg acg gtt att cga ggc	1075
Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu Thr Val Ile Arg Gly	
310 315 320 325	
act gat gag cag ctc gtt gag gta tta gag cag ttg cca cgt act cgg	1123
Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln Leu Pro Arg Thr Arg	
330 335 340	
gtg att gtg gct cct cat gcg gcg gat ctt ttt gat caa agt gtc agg	1171
Val Ile Val Ala Pro His Ala Ala Asp Leu Phe Asp Gln Ser Val Arg	
345 350 355	
gac aat gtg cat ccc gtg gca gag gtc gcg gag aaa gcc att gaa gtt	1219
Asp Asn Val His Pro Val Ala Glu Val Ala Glu Lys Ala Ile Glu Val	

360	365	370	
gcc tcc tgt gac gat att cca ggt ggt agt tcc aag att gtg ggc gag			1267
Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser Lys Ile Val Gly Glu			
375	380	385	
ggt gga cgg ttg ctc tcg ggt ggt cag cgt cag cgc gtt gca ctg gct			1315
Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala			
390	395	400	405
cgg gcg att gct ttt gat cca gag gtg ttg gtg ctt caa gat ccc aca			1363
Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val Leu Gln Asp Pro Thr			
410	415	420	
acg gca gtg gat tct gtg acg gag caa aac att gct cag caa gtg gca			1411
Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile Ala Gln Gln Val Ala			
425	430	435	
gca cac cgt gca gga aaa gtg acc att gtg ttt agt gag gca ccc gcg			1459
Ala His Arg Ala Gly Lys Val Thr Ile Val Phe Ser Glu Ala Pro Ala			
440	445	450	
tgg agt gcg gtg gct gat caa cac gtt gag gca gct gct ttg cgg gag			1507
Trp Ser Ala Val Ala Asp Gln His Val Glu Ala Ala Ala Leu Arg Glu			
455	460	465	
ggt atg aaa tgagtgggga gacgtcgaaa agc			1539
Val Met Lys			
470			

<210> 282

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Ala Ser Ala Gly Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr			
1	5	10	15
Pro Val Ile Val Gly Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp			
20	25	30	
Leu Gln Arg Leu Trp Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu			
35	40	45	
Thr Ala Met Thr Val Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser			
50	55	60	
Gln Gln Leu Val Ser His Asp Leu Arg Met Leu Val Thr Asp Arg Ile			
65	70	75	80
Gln Asp Pro Arg Gly Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu			
85	90	95	
Leu Ser Ile Ala Ser Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met			
100	105	110	

Met Thr Val Phe Pro Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala
 115 120 125
 Val Val Met Tyr Ser Ile Asn Pro Trp Leu Ser Val Ala Val Leu Il
 130 135 140
 Gly Gly Pro Leu Leu Val Val Val Ala Ile Gln Val Ser Lys Pro Leu
 145 150 155 160
 Gln Lys Arg Ser Gly Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala
 165 170 175
 Thr Ala Thr Asp Val Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly
 180 185 190
 Ala Ile Val Thr Val Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala
 195 200 205
 Tyr Arg Lys Thr Val His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly
 210 215 220
 Val Thr Asp Ala Ala Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly
 225 230 235 240
 Ala Gly Phe Leu Ala Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile
 245 250 255
 Thr Val Val Gly Leu Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu
 260 265 270
 Gly Arg Asn Val Ala Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys
 275 280 285
 Arg Ile Arg Gly Val Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His
 290 295 300
 Asp Ala Asp Lys Ala Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu
 305 310 315 320
 Thr Val Ile Arg Gly Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln
 325 330 335
 Leu Pro Arg Thr Arg Val Ile Val Ala Pro His Ala Ala Asp Leu Phe
 340 345 350
 Asp Gln Ser Val Arg Asp Asn Val His Pro Val Ala Glu Val Ala Glu
 355 360 365
 Lys Ala Ile Glu Val Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser
 370 375 380
 Lys Ile Val Gly Glu Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln
 385 390 395 400
 Arg Val Ala Leu Ala Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val
 405 410 415

Leu Gln Asp Pro Thr Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile
 420 425 430

Ala Gln Gln Val Ala Ala His Arg Ala Gly Lys Val Thr Ile Val Phe
 435 440 445

Ser Glu Ala Pro Ala Trp Ser Ala Val Ala Asp Gln His Val Glu Ala
 450 455 460

Ala Ala Leu Arg Glu Val Met Lys
 465 470

<210> 283

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXN01190

<400> 283

cagggttttg atgagaacaa cacacaccgc ttcaagcatt ctgcgaagaa tgatcaggcg 60

gcagcggggc aaggttgcgt ttggcgcatt ctttttgggg atg tgg cag ctg tcg 115
 Met Trp Gln Leu Ser
 1 5

gaa gca ttg gtg ccg att gcg att ggt ttg atc gtt gat cat gcg gtt 163
 Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile Val Asp His Ala Val
 10 15 20

ctc aca aaa gat ctc cgc cga tta gtg gtc ggg ctt gtc gct ttt gtt 211
 Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly Leu Val Ala Phe Val
 25 30 35

gtg ctg ttt gtg gtg ttg agt ttt tct aat cgt ttc ggt tcg cgc gcg 259
 Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg Phe Gly Ser Arg Ala
 40 45 50

ttg aat agg gcc gtg aac ttt gaa tcc cat gcg ctc cgc gta gag gta 307
 Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala Leu Arg Val Glu Val
 55 60 65

gcc gat cat gcg ttg aag aat ctg gat ccg cgc aat ttg gtg cct ggc 355
 Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg Asn Leu Val Pro Gly
 70 75 80 85

gag gtg atg tcg cgg tcc acc gca gat gcg gat tct tcg acg cgt att 403
 Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp Ser Ser Thr Arg Ile
 90 95 100

ttc ggg cag atc gga acc ggt gtt tcg gct gcg acg gga ttt ctt ggt 451
 Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala Thr Gly Phe Leu Gly

105	110	115	
gca gcg acc tac ctg ttg atc agt gac tgg ctg gtc ggg ttg ttg gtg Ala Ala Thr Tyr Leu Leu Ile Ser Asp Trp Leu Val Gly Leu Leu Val 120 125 130			499
ctt gtg ctg gta ccg atc att tcg gga gtg gtt gca ctg gct agc aag Leu Val Leu Val Pro Ile Ile Ser Gly Val Val Ala Leu Ala Ser Lys 135 140 145			547
ggc att tct aaa agg agt gtc acc cag cag gag aag ttg gcg gag tct Gly Ile Ser Lys Arg Ser Val Thr Gln Gln Glu Lys Leu Ala Glu Ser 150 155 160 165			595
ggt gcg cag gca agt gac atc atg atg ggg ctg cgc gtg atc aag gcg Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu Arg Val Ile Lys Ala 170 175 180			643
atc ggt ggc gag cgt tgg gcc gtg aag act ttt gaa aag gcg tcg cag Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe Glu Lys Ala Ser Gln 185 190 195			691
gca tca gcg aga gcg gcg gtt gat act gca gtt gct tcg ggc aaa gtc Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val Ala Ser Gly Lys Val 200 205 210			739
gct ggt att ggt gag ttg tcc att gcg gtg aat ttg gct gcg gtg ttg Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn Leu Ala Ala Val Leu 215 220 225			787
ttg ctt gct ggt tgg cgg gtc acc acg ggg gag ttg ggg cct ggc cag Leu Leu Ala Gly Trp Arg Val Thr Thr Gly Glu Leu Gly Pro Gly Gln 230 235 240 245			835
ttg atc gca att gtg ggt gtg gcg gtg tat ttg tca gag ccg att cgc Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu Ser Glu Pro Ile Arg 250 255 260			883
ttg ctg agc aac tcg att aat gcc tca gct att gcg cac ggt gca gcg Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile Ala His Gly Ala Ala 265 270 275			931
gag cgg gtg gct aat ttc tta aac ctc gac gaa tct cag gca cag tac Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu Ser Gln Ala Gln Tyr 280 285 290			979
gaa agc agc gaa aca atc aat gac ggc gaa ttc ctc gtc atc gtg ccc Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe Leu Val Ile Val Pro 295 300 305			1027
cca gcc agc acg ctt cca cac ggc gac aat atc ttg gct aca cct cat Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile Leu Ala Thr Pro His 310 315 320 325			1075
gct gcc gac att ttc gaa ggt acc ttg cgg tca aat att tcc atg aat Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser Asn Ile Ser Met Asn 330 335 340			1123

cat gag gac aac gtg cca att gat ccg cag gta att cgc gct tct ggt 1171
 His Glu Asp Asn Val Pro Ile Asp Pro Gln Val Ile Arg Ala Ser Gly
 345 350 355
 ctg act gac atc att gag gtg gac gga ctt gat gcg ccg gtg cgc gat 1219
 Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp Ala Pro Val Arg Asp
 360 365 370
 acg gga agc aat tta tcg ggt ggg cag cgt cag cga gtg gct ttg gcc 1267
 Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala
 375 380 385
 agg gcg ttg cat gca gac gcg gaa gta ctg gtg ctg atg gat cca acc 1315
 Arg Ala Leu His Ala Asp Ala Glu Val Leu Val Leu Met Asp Pro Thr
 390 395 400 405
 agc gcg gtg gat tca gtg acg gag gtg tct atc gcg cag ggg att aag 1363
 Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile Ala Gln Gly Ile Lys
 410 415 420
 cag ctg cga gca ggc aaa acc acc att gtg gtg agt tct tcg ccc gcg 1411
 Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val Ser Ser Ser Pro Ala
 425 430 435
 ttt tac aac ttg gcg gat cgg gtg att tca cat gtc taatttgatg 1457
 Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His Val
 440 445
 gcatcatcga cac. 1470

<210> 284

<211> 449

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 284

Met Trp Gln Leu Ser Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile
 1 5 10 15
 Val Asp His Ala Val Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly
 20 25 30
 Leu Val Ala Phe Val Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg
 35 40 45
 Phe Gly Ser Arg Ala Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala
 50 55 60
 Leu Arg Val Glu Val Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg
 65 70 75 80
 Asn Leu Val Pro Gly Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp
 85 90 95
 Ser Ser Thr Arg Ile Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala

100										105					110						
Thr	Gly	Phe	Leu	Gly	Ala	Ala	Thr	Tyr	Leu	Leu	Ile	Ser	Asp	Trp	Leu						
		115						120					125								
Val	Gly	Leu	Leu	Val	Leu	Val	Leu	Val	Pro	Ile	Ile	Ser	Gly	Val	Val						
		130				135					140										
Ala	Leu	Ala	Ser	Lys	Gly	Ile	Ser	Lys	Arg	Ser	Val	Thr	Gln	Gln	Glu						
		145			150					155					160						
Lys	Leu	Ala	Glu	Ser	Gly	Ala	Gln	Ala	Ser	Asp	Ile	Met	Met	Gly	Leu						
				165					170					175							
Arg	Val	Ile	Lys	Ala	Ile	Gly	Gly	Glu	Arg	Trp	Ala	Val	Lys	Thr	Phe						
			180					185					190								
Glu	Lys	Ala	Ser	Gln	Ala	Ser	Ala	Arg	Ala	Ala	Val	Asp	Thr	Ala	Val						
		195					200					205									
Ala	Ser	Gly	Lys	Val	Ala	Gly	Ile	Gly	Glu	Leu	Ser	Ile	Ala	Val	Asn						
		210				215					220										
Leu	Ala	Ala	Val	Leu	Leu	Leu	Ala	Gly	Trp	Arg	Val	Thr	Thr	Gly	Glu						
		225			230				235						240						
Leu	Gly	Pro	Gly	Gln	Leu	Ile	Ala	Ile	Val	Gly	Val	Ala	Val	Tyr	Leu						
				245					250					255							
Ser	Glu	Pro	Ile	Arg	Leu	Leu	Ser	Asn	Ser	Ile	Asn	Ala	Ser	Ala	Ile						
			260					265					270								
Ala	His	Gly	Ala	Ala	Glu	Arg	Val	Ala	Asn	Phe	Leu	Asn	Leu	Asp	Glu						
		275					280					285									
Ser	Gln	Ala	Gln	Tyr	Glu	Ser	Ser	Glu	Thr	Ile	Asn	Asp	Gly	Glu	Phe						
		290				295					300										
Leu	Val	Ile	Val	Pro	Pro	Ala	Ser	Thr	Leu	Pro	His	Gly	Asp	Asn	Ile						
		305			310					315				320							
Leu	Ala	Thr	Pro	His	Ala	Ala	Asp	Ile	Phe	Glu	Gly	Thr	Leu	Arg	Ser						
				325					330					335							
Asn	Ile	Ser	Met	Asn	His	Glu	Asp	Asn	Val	Pro	Ile	Asp	Pro	Gln	Val						
			340					345					350								
Ile	Arg	Ala	Ser	Gly	Leu	Thr	Asp	Ile	Ile	Glu	Val	Asp	Gly	Leu	Asp						
		355					360					365									
Ala	Pro	Val	Arg	Asp	Thr	Gly	Ser	Asn	Leu	Ser	Gly	Gly	Gln	Arg	Gln						
		370				375					380										
Arg	Val	Ala	Leu	Ala	Arg	Ala	Leu	His	Ala	Asp	Ala	Glu	Val	Leu	Val						
		385			390					395				400							
Leu	Met	Asp	Pro	Thr	Ser	Ala	Val	Asp	Ser	Val	Thr	Glu	Val	Ser	Ile						

405

410

415

Ala Gln Gly Ile Lys Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val
 420 425 430

Ser Ser Ser Pro Ala Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His
 435 440 445

Val

<210> 285

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> RXN01102

<400> 285

attctatggt tgttgggaga gatgacttaa tttggaatca cgggctttaa cacgcgctga 60

cattgagcaa cttcccagca tgtggaaaag cccaggtttc gtg gct gtc ctc gtg 115
 Val Ala Val Leu Val
 1 5

gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta 163
 Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val
 10 15 20

ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc 211
 Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala
 25 30 35

acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act 259
 Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr
 40 45 50

ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc 307
 Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala
 55 60 65

gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag 355
 Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu
 70 75 80 85

cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt 403
 Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly
 90 95 100

gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta 451
 Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val
 105 110 115

cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt	499
Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu	
120 125 130	
tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt	547
Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe	
135 140 145	
ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca	595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala	
150 155 160 165	
gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag	643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Ala Lys Gln	
170 175 180	
caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg	691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu	
185 190 195	
gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc	739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly	
200 205 210	
gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga	787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly	
215 220 225	
tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct	835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser	
230 235 240 245	
tca atg gtg ttc cgc tac ctg tcc gcc gtt atc gct gac cgc cgc ggt	883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly	
250 255 260	
gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt	931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly	
265 270 275	
gtc gtt tta atc acc gtc aca atc ttc caa gcc tgg tcc gtg tgg ctt	979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu	
280 285 290	
ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt gcc atg gtg caa	1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln	
295 300 305	
aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc	1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val	
310 315 320 325	
tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga	1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly	
330 335 340	
atc gga agc ttc ctc ctt ggc ata gtt gcc gca tcg ctt gct tac agt	1171

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Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser
      345                      350                      355

ggt gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg      1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu
      360                      365                      370

acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac      1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn
      375                      380                      385

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg      1315
Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
      390                      395                      400                      405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcca      1365
Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
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ccc                                                                1368

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<212> PRT
<213> Corynebacterium glutamicum

<400> 286
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Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
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Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
      35                      40                      45

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
      50                      55                      60

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
      65                      70                      75                      80

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
      85                      90                      95

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
      100                      105                      110

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
      115                      120                      125

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
      130                      135                      140

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
      145                      150                      155                      160

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Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
 165 170 175
 Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
 180 185 190
 Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
 195 200 205
 Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
 210 215 220
 Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
 225 230 235 240
 Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
 245 250 255
 Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
 260 265 270
 Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
 275 280 285
 Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
 290 295 300
 Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
 305 310 315 320
 Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
 325 330 335
 Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
 340 345 350
 Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
 355 360 365
 Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
 370 375 380
 Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
 385 390 395 400
 Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
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<210> 287

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(325)

<223> RXN00788

<400> 287

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 Met Ala Ser Ser Ile
 1 5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct 163
 Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
 10 15 20

ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt 211
 Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
 25 30 35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg 259
 Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
 40 45 50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg 307
 Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
 55 60 65

gag cac cag ccc gcc caa taaataattt ctctcttcta att 348
 Glu His Gln Pro Ala Gln
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<210> 288

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

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Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
 35 40 45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
 50 55 60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
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<210> 289

<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1741)

<223> RXN02119

<400> 289

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gcttaaattg cttgtcgacg cctagtgcc caatggagac atg acc gaa aca ctt 115
 Met Thr Glu Thr Leu
 1 5

gtg gtg aat ggc ctt gca ggc ggc tat ggg cac cgc aca tta ttt aac 163
 Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His Arg Thr Leu Phe Asn
 10 15 20

gat gtg aat ctc acc gta gct gcc ggc gat gtc gtg ggc gtt gtc ggc 211
 Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val Val Gly Val Val Gly
 25 30 35

gtc aat ggc gct ggt aaa tcc aca ttt cta aaa att ctg gcg ggc gtg 259
 Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ala Gly Val
 40 45 50

gaa aag cca ctg gct gga act atc gcg ctt tcg cca gcc gat gct ttt 307
 Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser Pro Ala Asp Ala Phe
 55 60 65

gtg ggc tac ttg cca cag gaa cac acc cgc acg tct gga gag acg atc 355
 Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr Ser Gly Glu Thr Ile
 70 75 80 85

gca gtt tac att gct cgt cga acc ggc tgc caa gct gca aca act gcc 403
 Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln Ala Ala Thr Thr Ala
 90 95 100

atg gat gac acc gcc gaa gcg ttt ggt gcg gat cca gac aac gct gcc 451
 Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp Pro Asp Asn Ala Ala
 105 110 115

ttg gcc gat gca tac gcc gag gcg ctg gat cgg tgg atg gcc agt ggc 499
 Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg Trp Met Ala Ser Gly
 120 125 130

gca gcc gat ttg gat gaa cgc atc ccc atc gtg ctc gct gat ttg ggc 547
 Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val Leu Ala Asp Leu Gly
 135 140 145

ttt gag ctt ccc acc tcg acg ctg atg gaa gga ctt tca ggc ggc cag 595
 Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly Leu Ser Gly Gly Gln
 150 155 160 165

gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att 643
 Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile
 170 175 180

gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag	691
Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu	
185 190 195	
caa ctg gag aat ttt gtt cag ggg ctt cgc ggg gga gtc gta ctg gtc	739
Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val	
200 205 210	
agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa	787
Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu	
215 220 225	
ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat	835
Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp	
230 235 240 245	
tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa	883
Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln	
250 255 260	
tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga	931
Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg	
265 270 275	
acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt	979
Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg	
280 285 290	
gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt	1027
Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Glu Ser Ser	
295 300 305	
gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg	1075
Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg	
310 315 320 325	
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Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser	
330 335 340	
gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat	1171
Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val Ser Thr Leu Asn Asp	
345 350 355	
gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa	1219
Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln	
360 365 370	
gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt	1267
Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly	
375 380 385	
aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc	1315
Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser	
390 395 400 405	
ggg act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag	1363

Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln
 410 415 420

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa 1411
 Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu
 425 430 435

aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg 1459
 Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala
 440 445 450

aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta 1507
 Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu
 455 460 465

tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg 1555
 Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg
 470 475 480 485

ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg 1603
 Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr Asn His Leu Asp Leu
 490 495 500

gag gcc atc gag caa ttg gag caa gcg ttg gcc tcg tat gat ggt gtg 1651
 Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala Ser Tyr Asp Gly Val
 505 510 515

ttg ctg ctg gtc acg cac gat cgt cgc atg ttg gac gct gtg cag acc 1699
 Leu Leu Leu Val Thr His Asp Arg Arg Met Leu Asp Ala Val Gln Thr
 520 525 530

aat cgt cgt tgg cat gtc gag gct ggc gaa gtt agg gag cta 1741
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taaccgtttc cgtattgatg cca 1764

<210> 290

<211> 547

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val
 20 25 30

Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys
 35 40 45

Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser
 50 55 60

Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr

65	70	75	80
Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln	85	90	95
Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp	100	105	110
Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg	115	120	125
Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val	130	135	140
Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly	145	150	155
Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu	165	170	175
Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp	180	185	190
Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly	195	200	205
Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val	210	215	220
Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr	225	230	235
Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln	245	250	255
His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu	260	265	270
Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg	275	280	285
Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala	290	295	300
Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu	305	310	315
Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp	325	330	335
Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val	340	345	350
Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly	355	360	365
Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly			

370

375

380

Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn
 385 390 395 400

Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile
 405 410 415

Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu
 420 425 430

Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val
 435 440 445

Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg
 450 455 460

Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala
 465 470 475 480

Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr
 485 490 495

Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala
 500 505 510

Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu
 515 520 525

Asp Ala Val Gln Thr Asn Arg Arg Trp His Val Glu Ala Gly Glu Val
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Arg Glu Leu
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<210> 291

<211> 1638

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1615)

<223> RXN01605

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 Val Thr Ser Asp Ser
 1 5

ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc 163
 Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
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Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr	
25 30 35	
atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt	259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly	
40 45 50	
ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act	307
Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr	
55 60 65	
acg ctc agc gat ggc gtc ggt tcc gcc aac gac ggt gca gtt cag ctt	355
Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu	
70 75 80 85	
gcc gac ggc gcg gtc acc ctg cgc gac ggc atc gca agt gcc aat gag	403
Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu	
90 95 100	
ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc	451
Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu	
105 110 115	
ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc	499
Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala Asp Gly Leu Ser Ser	
120 125 130	
ctg tct gcg ggc acc gcc caa cta ggc caa ggc gca acc cag gtt tca	547
Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly Ala Thr Gln Val Ser	
135 140 145	
gat ggc gtg ggc caa ctt gtc gac caa gta gca cca ctg acc gcc tat	595
Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala Pro Leu Thr Ala Tyr	
150 155 160 165	
gtt cca gac atc aac tct cag ttg atc acc ctg cgc gac ggc gca gcc	643
Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu Arg Asp Gly Ala Ala	
170 175 180	
acc att gcc tct gaa cta tct gat ccc tcc agc acc tac cgc tcc ggc	691
Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser Thr Tyr Arg Ser Gly	
185 190 195	
gtg gac tcc gct gtg agc gca tcc cag caa cta gca gcc ggc ctg caa	739
Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu Ala Ala Gly Leu Gln	
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acc ctg aaa gac gga tcc agc caa ctc agc atc ggt gca cgc acc ctc	787
Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile Gly Ala Arg Thr Leu	
215 220 225	
gct gat ggc acc agc caa ttg gcc gca ggt tcc gaa cag cta gtt gtt	835
Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser Glu Gln Leu Val Val	
230 235 240 245	
ggc gca caa gca ctg cgc gac ggc acc gtc cag ctt gat gaa ggc tcc	883

Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln Leu Asp Glu Gly Ser	
250 255 260	
agc gaa ctc gcc ctc aaa ctc acc gac ggc gca agc caa gta cca acc	931
Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala Ser Gln Val Pro Thr	
265 270 275	
ttc gct gac ggc gca gac acc acc atc gca acc cca gtt gaa aca gaa	979
Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr Pro Val Glu Thr Glu	
280 285 290	
caa gca gga gac acc aca ccg ctc ttc ggt att ggt ctc gca cca ttc	1027
Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile Gly Leu Ala Pro Phe	
295 300 305	
ttc atg gct gtc ggc ctg ttc atg gga gca acc gtt gcc tgg atg atc	1075
Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr Val Ala Trp Met Ile	
310 315 320 325	
ctg cac cca atc agt cgc cgc gca ctc gac tcc cgc atg gga ggc ttc	1123
Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser Arg Met Gly Gly Phe	
330 335 340	
cga ggc acc ctg gca agc tac ctt cca tca aca gtc tta ggc ctt ggc	1171
Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr Val Leu Gly Leu Gly	
345 350 355	
caa gca acc atc atg tgg gca gta ctg tac ttc ctg ctc gac ctc aat	1219
Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe Leu Leu Asp Leu Asn	
360 365 370	
cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg	1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met Val Ala Ile Ser Trp	
375 380 385	
gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc	1315
Val Phe Ile Ser Ile Thr His Met Phe Asn Asn Val Ala Gly Pro Ser	
390 395 400 405	
gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc	1363
Ala Gly Arg Val Leu Ser Ile Val Met Met Ser Phe Gln Leu Val Ser	
410 415 420	
tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg	1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro Ala Phe Phe His Trp	
425 430 435	
ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa	1459
Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val Asn Leu Val Arg Gln	
440 445 450	
atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca	1507
Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro Arg Phe Ile Gln Ala	
455 460 465	
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Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met Leu Ala Ile Ser Thr	

470 475 480 485

ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca 1603
 Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met Lys Asp Tyr His Pro
 490 495 500

gaa ctg aag gtc taaaagcttt tcccgcccg ttc 1638
 Glu Leu Lys Val
 505

<210> 292
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 292
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Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
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Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
 35 40 45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
 50 55 60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
 65 70 75 80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
 85 90 95

Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
 100 105 110

Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
 115 120 125

Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
 130 135 140

Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
 145 150 155 160

Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
 165 170 175

Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser
 180 185 190

Thr Tyr Arg Ser Gly Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu
 195 200 205

Ala Ala Gly Leu Gln Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile

210	215	220
Gly Ala Arg Thr Leu 225	Ala Asp Gly Thr 230	Ser Gln Leu Ala Ala Gly Ser 235 240
Glu Gln Leu Val 245	Val Gly Ala Gln Ala 250	Leu Arg Asp Gly Thr Val Gln 255
Leu Asp Glu Gly Ser Ser Glu Leu Ala 260	Leu Lys Leu Thr Asp Gly Ala 265 270	
Ser Gln Val Pro Thr Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr 275 280 285		
Pro Val Glu Thr Glu Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile 290 295 300		
Gly Leu Ala Pro Phe Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr 305 310 315 320		
Val Ala Trp Met Ile Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser 325 330 335		
Arg Met Gly Gly Phe Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr 340 345 350		
Val Leu Gly Leu Gly Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe 355 360 365		
Leu Leu Asp Leu Asn Pro Ala His Pro Ala Gly Leu Trp Met Ala Met 370 375 380		
Val Ala Ile Ser Trp Val Phe Ile Ser Ile Thr His Met Phe Asn Asn 385 390 395 400		
Val Ala Gly Pro Ser Ala Gly Arg Val Leu Ser Ile Val Met Met Ser 405 410 415		
Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro 420 425 430		
Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val 435 440 445		
Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro 450 455 460		
Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met 465 470 475 480		
Leu Ala Ile Ser Thr Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met 485 490 495		
Lys Asp Tyr His Pro Glu Leu Lys Val 500 505		

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Met Val Pro Asn Thr 5																
1																
gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163																
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg 20																
10																
15																
ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211																
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro 35																
25																
30																
35																
tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259																
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu 50																
40																
45																
50																
gaa ggc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307																
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu 65																
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cta cgc ggc gag ttg ggc gat ttg ctg ttt cag acc gtg ttt cac gcc 355																
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70																
75																
80																
85																
caa atg gcg cgc gag gca ggc cat ttc gct ttg gtt gac gtg gtg aag 403																
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys 100																
90																
95																
100																
gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc ggc gcg 451																
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala 115																
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Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Glu Asp Trp Glu Val 130																
120																
125																
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Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln Lys Gly Val Leu Asp 145																
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ggc gtc gcg ctg gga ctg cct gcc ctg atg cgc gcg acg aag ctg caa 595																
Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg Ala Thr Lys Leu Gln 165																
150																
155																
160																
165																

aac aac gcc gcg cgc gtt ggg ttt gat tgg ccc gac att ggg cag gta 643
 Asn Asn Ala Ala Arg Val Gly Phe Asp Trp Pro Asp Ile Gly Gln Val
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 Leu Gly Lys Val Thr Glu Glu
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<210> 294

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met Val Pro Asn Thr Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala
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Thr Gln Ile Gln Arg Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro
 20 25 30

Val Ser Gly Cys Pro Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala
 35 40 45

Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
 50 55 60

Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
 65 70 75 80

Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
 85 90 95

Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
 100 105 110

His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
 115 120 125

Glu Asp Trp Glu Val Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln
 130 135 140

Lys Gly Val Leu Asp Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg
 145 150 155 160

Ala Thr Lys Leu Gln Asn Asn Ala Ala Arg Val Gly Phe Asp Trp Pro
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Asp Ile Gly Gln Val Leu Gly Lys Val Thr Glu Glu
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<210> 295

<211> 357

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXS02979

<400> 295

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 Met Thr Ala Pro Asn
 1 5

act ctc aag caa aca act ctt cgc tct gat gag ttc tct tgc cca tcc 163
 Thr Leu Lys Gln Thr Thr Leu Arg Ser Asp Glu Phe Ser Cys Pro Ser
 10 15 20

tgt gtc tcc aag att gaa aac aaa ttg aat gga ttg gat ggc gtc gac 211
 Cys Val Ser Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Asp
 25 30 35

aat gca gag gtg aag ttc tcc tcc gga aga atc ctt gtt gat cac gac 259
 Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Val Asp His Asp
 40 45 50

ccc agc aag gtc tct atc aag gat cta gtc gct gca gtc gca gag gtt 307
 Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala Ala Val Ala Glu Val
 55 60 65

ggc tac acc gca aag cca tca gca atc taaaactctc agttagacca 354
 Gly Tyr Thr Ala Lys Pro Ser Ala Ile
 70 75

tta 357

<210> 296

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Met Thr Ala Pro Asn Thr Leu Lys Gln Thr Thr Leu Arg Ser Asp Glu
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Phe Ser Cys Pro Ser Cys Val Ser Lys Ile Glu Asn Lys Leu Asn Gly
 20 25 30

Leu Asp Gly Val Asp Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile
 35 40 45

Leu Val Asp His Asp Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala
 50 55 60

Ala Val Ala Glu Val Gly Tyr Thr Ala Lys Pro Ser Ala Ile
 65 70 75


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Phe Thr Cys Pro Ser Cys Val Ala Lys Ile Glu Asn Lys Leu Asn Gly
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Leu Asp Gly Val Glu Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile
      35              40              45

Leu Ile Thr His Asp Pro Gln Lys Val Ser Val Arg Asp Leu Val Thr
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Ala Val Ala Glu Val Gly Tyr Thr Ala Lys Pro Ser Ala Ile
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 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Asn Ala Asp Lys
 1 5
 aaa atg tgc gga atg aac ccg gat agc caa tac gtc gaa ctt gcc gtc 163
 Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr Val Glu Leu Ala Val
 10 15 20
 gaa gtt ttc gga ctc ctc gcg gac gcc act cga gtt cgc atc atc ttg 211
 Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg Val Arg Ile Ile Leu
 25 30 35
 gca ctt cga aac agt ggt gaa ctt tcc gta aac cac ctc gcg gac atc 259
 Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn His Leu Ala Asp Ile
 40 45 50
 gtc gat aaa tcc ccc gca gca gtt tcc caa cac ctc gcc cgg ctg cgc 307
 Val Asp Lys Ser Pro Ala Ala Val Ser Gln His Leu Ala Arg Leu Arg
 55 60 65
 atg gcc cga atc gtg tcc acc cgt caa gaa ggt caa cga gtt ttc tac 355
 Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly Gln Arg Val Phe Tyr
 70 75 80 85
 aaa ctc acc aat gaa cac gca tca cag cta gtc tcc gac gct att ttt 403
 Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val Ser Asp Ala Ile Phe
 90 95 100
 cag gcg gaa cac acc att gcg gac ggc cag act ccc cca cac cac cac 451
 Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr Pro Pro His His His
 105 110 115
 cga gaa cga gaa caa tca tgaccaccca cagtcaccaa gaa 492
 Arg Glu Arg Glu Gln Ser
 120

<210> 300
 <211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Asn Ala Asp Lys Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr
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Val Glu Leu Ala Val Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg
 20 25 30

Val Arg Ile Ile Leu Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn
 35 40 45

His Leu Ala Asp Ile Val Asp Lys Ser Pro Ala Ala Val Ser Gln His
 50 55 60

Leu Ala Arg Leu Arg Met Ala Arg Ile Val Ser Thr Asp Gln Glu Gly
 65 70 75 80

Gln Arg Val Phe Tyr Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val
 85 90 95

Ser Asp Ala Ile Phe Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr
 100 105 110

Pro Pro His His His Arg Glu Arg Glu Gln Ser
 115 120

<210> 301

<211> 10

<212> PRT

<213> Corynebacterium glutamicum

<400> 301

Ala Pro Ala Leu Gly Pro Thr Leu Ser Gly
 1 5 10

<210> 302

<211> 10

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Gly Xaa Xaa Xaa Gly Pro Xaa Xaa Gly Gly
 1 5 10

<210> 303

<211> 20

<212> DNA

<213> Corynebacterium glutamicum

<400> 303

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20

<210> 304
<211> 20
<212> DNA
<213> *Corynebacterium glutamicum*

<400> 304
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BGI-124CPPC - 97 -

20